

21569YP



SEQUENCE LISTING

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<120> POLYPEPTIDES FOR INDUCING A PROTECTIVE  
IMMUNE RESPONSE AGAINST STAPHYLOCOCCUS AUREUS

<130> 21569YP

<140> US 10/564,458  
<141> 2006-01-12

<150> PCT/2004/023523  
<151> 2004-07-22

<150> 60/489,840  
<151> 2003-07-24

<150> 60/520,115  
<151> 2003-11-14

<160> 109

<170> FastSEQ for Windows Version 4.0

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<211> 446  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> ORF0657nI with amino terminus methionine

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Glu Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr  
20 25 30  
Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala  
35 40 45  
Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala  
50 55 60  
Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn  
65 70 75 80  
Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro  
85 90 95  
Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp  
100 105 110

Phe Glu Met Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala  
 115 120 125  
 Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu  
 130 135 140  
 Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val  
 145 150 155 160  
 Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr  
 165 170 175  
 Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys  
 180 185 190  
 Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys  
 195 200 205  
 Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala  
 210 215 220  
 Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala  
 225 230 235 240  
 Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn  
 245 250 255  
 Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys  
 260 265 270  
 Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala  
 275 280 285  
 Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp  
 290 295 300  
 Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu  
 305 310 315 320  
 Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu  
 325 330 335  
 Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp  
 340 345 350  
 Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp  
 355 360 365  
 Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys  
 370 375 380  
 Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr  
 385 390 395 400  
 Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys  
 405 410 415  
 Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala  
 420 425 430  
 Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro  
 435 440 445

<210> 2  
 <211> 645  
 <212> PRT  
 <213> S. aureus

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 Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys  
 1 5 10 15  
 Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu  
 20 25 30

Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr  
 35 40 45  
 Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr  
 50 55 60  
 Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser  
 65 70 75 80  
 Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala  
 85 90 95  
 Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys  
 100 105 110  
 Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu  
 115 120 125  
 Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser  
 130 135 140  
 Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly  
 145 150 155 160  
 Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val  
 165 170 175  
 Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly  
 180 185 190  
 Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro  
 195 200 205  
 Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg  
 210 215 220  
 Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr  
 225 230 235 240  
 His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe  
 245 250 255  
 Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp  
 260 265 270  
 Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu  
 275 280 285  
 Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu  
 290 295 300  
 Lys Leu Lys Ala Glu Tyr Lys Lys Leu Glu Asp Thr Lys Lys Ala  
 305 310 315 320  
 Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln  
 325 330 335  
 Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val  
 340 345 350  
 Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys  
 355 360 365  
 His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met  
 370 375 380  
 Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln  
 385 390 395 400  
 Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile  
 405 410 415  
 Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys  
 420 425 430  
 Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile  
 435 440 445  
 Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys  
 450 455 460

Lys Glu Gln Gln Asp Asn Ser Ala Lys Glu Ala Thr Pro Ala Thr  
 465 470 475 480  
 Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln  
 485 490 495  
 Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu  
 500 505 510  
 Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys  
 515 520 525  
 Pro Thr Lys Gly Glu Val Glu Ser Ser Thr Thr Pro Thr Lys Val  
 530 535 540  
 Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys  
 545 550 555 560  
 Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys  
 565 570 575  
 Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly  
 580 585 590  
 His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys  
 595 600 605  
 Ser Leu Pro Gln Thr Gly Glu Ser Asn Lys Asp Met Thr Leu Pro  
 610 615 620  
 Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro  
 625 630 635 640  
 Arg Lys Arg Lys Asn  
 645

<210> 3  
 <211> 569  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH with amino terminus methionine

<400> 3  
 Met Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr  
 1 5 10 15  
 Glu Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr  
 20 25 30  
 Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala  
 35 40 45  
 Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala  
 50 55 60  
 Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn  
 65 70 75 80  
 Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro  
 85 90 95  
 Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp  
 100 105 110  
 Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala  
 115 120 125  
 Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu  
 130 135 140  
 Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val  
 145 150 155 160

Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr  
 165 170 175  
 Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys  
 180 185 190  
 Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys  
 195 200 205  
 Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala  
 210 215 220  
 Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala  
 225 230 235 240  
 Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn  
 245 250 255  
 Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys  
 260 265 270  
 Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala  
 275 280 285  
 Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp  
 290 295 300  
 Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu  
 305 310 315 320  
 Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu  
 325 330 335  
 Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp  
 340 345 350  
 Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp  
 355 360 365  
 Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys  
 370 375 380  
 Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr  
 385 390 395 400  
 Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys  
 405 410 415  
 Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala  
 420 425 430  
 Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro  
 435 440 445  
 Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys  
 450 455 460  
 Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly  
 465 470 475 480  
 Lys Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser  
 485 490 495  
 Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala  
 500 505 510  
 Lys Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr  
 515 520 525  
 Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala  
 530 535 540  
 Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys  
 545 550 555 560  
 Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 565

<210> 4  
 <211> 570  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH with amino terminus methionine-glycine

<400> 4  
 Met Gly Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys  
 1 5 10 15  
 Thr Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu  
 20 25 30  
 Thr Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu  
 35 40 45  
 Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys  
 50 55 60  
 Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn  
 65 70 75 80  
 Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn  
 85 90 95  
 Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile  
 100 105 110  
 Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr  
 115 120 125  
 Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro  
 130 135 140  
 Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu  
 145 150 155 160  
 Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp  
 165 170 175  
 Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr  
 180 185 190  
 Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu  
 195 200 205  
 Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser  
 210 215 220  
 Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu  
 225 230 235 240  
 Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu  
 245 250 255  
 Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys  
 260 265 270  
 Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser  
 275 280 285  
 Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr  
 290 295 300  
 Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn  
 305 310 315 320  
 Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met  
 325 330 335  
 Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr  
 340 345 350  
 Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys  
 355 360 365

Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly
370					375					380					
Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp
385					390					395					400
Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr
					405					410					415
Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser
					420					425					430
Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser
					435					440					445
Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn
					450					455					460
Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser
465						470					475				480
Gly	Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu
						485					490				495
Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val
						500					505				510
Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln
						515					520				525
Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys
						530					535				540
Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn
						545					550				560
Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser						
					565					570					

<210> 5  
<211> 447  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> ORF0657nH with amino terminus methionine-glycine

Met	Gly	Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys
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Thr	Glu	Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu
						20				25					30
Thr	Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu
						35				40					45
Ala	Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys
						50				55					60
Ala	Pro	Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn
						65				70					80
Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn
						85				90					95
Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile
						100				105					110
Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr
							115			120					125
Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro
						130				135					140

Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu  
 145 150 155 160  
 Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp  
 165 170 175  
 Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr  
 180 185 190  
 Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu  
 195 200 205  
 Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser  
 210 215 220  
 Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu  
 225 230 235 240  
 Ala Pro Tyr Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu  
 245 250 255  
 Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys  
 260 265 270  
 Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser  
 275 280 285  
 Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr  
 290 295 300  
 Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn  
 305 310 315 320  
 Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met  
 325 330 335  
 Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr  
 340 345 350  
 Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys  
 355 360 365  
 Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly  
 370 375 380  
 Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp  
 385 390 395 400  
 Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr  
 405 410 415  
 Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser  
 420 425 430  
 Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro  
 435 440 445

<210> 6  
 <211> 576  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 6  
 Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
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 Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala  
 20 25 30  
 Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys  
 35 40 45

Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys  
 50 55 60  
 Ala Val Lys Glu Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro  
 65 70 75 80  
 Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu  
 85 90 95  
 Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala  
 100 105 110  
 Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr  
 115 120 125  
 Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile  
 130 135 140  
 Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln  
 145 150 155 160  
 Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile  
 165 170 175  
 Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe  
 180 185 190  
 Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His  
 195 200 205  
 Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala  
 210 215 220  
 Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr  
 225 230 235 240  
 Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu  
 245 250 255  
 Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys  
 260 265 270  
 Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu  
 275 280 285  
 Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro  
 290 295 300  
 Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr  
 305 310 315 320  
 Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Ala Phe Val Lys His  
 325 330 335  
 Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu  
 340 345 350  
 Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg  
 355 360 365  
 Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile  
 370 375 380  
 Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val  
 385 390 395 400  
 His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val  
 405 410 415  
 Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys  
 420 425 430  
 Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro  
 435 440 445  
 Ser Lys Pro Thr Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp  
 450 455 460  
 Ser Gln Lys Asp Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn  
 465 470 475 480

Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Met	Pro	Val	Thr	Lys	Pro
										485		490			495
Ala	Lys	Ala	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val
										500		505			510
Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Glu	Thr
										515		520			525
Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp
										530		535			540
Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His
										545		550			560
Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser
										565		570			575

<210> 7  
<211> 568  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> ORF0657nH

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1										5		10			15
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys
										20		25			30
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
										35		40			45
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
										50		55			60
Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr
										65		70			80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
										85		90			95
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
										100		105			110
Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
										115		120			125
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
										130		135			140
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
										145		150			160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
										165		170			175
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
										180		185			190
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
										195		200			205
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
										210		215			220
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
										225		230			240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
										245		250			255

Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Gly Val Thr Leu Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Gly Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys His Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

<210> 8  
 <211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

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 Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30

Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160  
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460

Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

<210> 9  
 <211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

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 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160  
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240

Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

<210> 10  
 <211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

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Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
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 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160  
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Lys Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445

Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln
450				455					460						
Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys
465				470					475			480			
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	Ser
														495	
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys
											500	505	510		
Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser
											515	520	525		
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn
											530	535	540		
Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn
											545	550	555	560	
Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser								
											565				

<210> 11  
 <211> 565  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

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1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys
									20	25				30	
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
									35	40				45	
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr
									50	55				60	
Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile
									65	70	75			80	
Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp
									85	90				95	
Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys
									100	105				110	
Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys
									115	120				125	
Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly
									130	135				140	
Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp
									145	150	155			160	
Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr
									165	170				175	
Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile
									180	185				190	
Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr
									195	200				205	
Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys
									210	215				220	

Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys  
 225 230 235 240  
 Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp  
 245 250 255  
 Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp  
 260 265 270  
 Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe  
 275 280 285  
 Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr  
 290 295 300  
 Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp  
 305 310 315 320  
 Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys  
 325 330 335  
 Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met  
 340 345 350  
 Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn  
 355 360 365  
 Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp  
 370 375 380  
 Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr  
 385 390 395 400  
 His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp  
 405 410 415  
 Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala  
 420 425 430  
 Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu  
 435 440 445  
 Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser  
 450 455 460  
 Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr  
 465 470 475 480  
 Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr  
 485 490 495  
 Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr  
 500 505 510  
 Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser  
 515 520 525  
 Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn  
 530 535 540  
 Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu  
 545 550 555 560  
 Asn Lys Ala Lys Ser  
 565

<210> 12  
 <211> 566  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 12

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
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 Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160  
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430

Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val
435						440					445				
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln
450						455					460				
Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys
465						470					475				480
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	Ser
										485	490			495	
Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro
										500	505			510	
Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly
										515	520			525	
Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys
										530	535			540	
Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln
										545	550			555	560
Glu	Asn	Lys	Ala	Lys	Ser										
						565									

<210> 13  
 <211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

Lys	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
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Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys
											20		25		30
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
											35		40		45
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
											50		55		60
Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr
											65		70		75
															80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
											85		90		95
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
											100		105		110
Glu	Met	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	
											115		120		125
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
											130		135		140
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
											145		150		155
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
											165		170		175
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
											180		185		190
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
											195		200		205

Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Lys Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

<210> 14  
 <211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 14

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
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 Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Glu  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160  
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Ala Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Ile Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415

Asn	Thr	Asp	Lys	Ser	Asn	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys		
420					425						430					
Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	
435					440						445					
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	
450					455						460					
Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	
465				470						475				480		
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser	
					485					490				495		
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Val	Lys	
						500					505				510	
Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	
						515					520				525	
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	
						530					535				540	
Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	
						545					550				560	
Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser									
						565										

<210> 15  
 <211> 564  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 15															
Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
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Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys
					20				25					30	
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
					35				40					45	
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr
					50				55					60	
Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile
					65				70					80	
Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp
					85				90					95	
Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys
					100				105					110	
Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys
					115				120					125	
Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly
					130				135					140	
Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp
					145				150					155	
Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr
					165				170					175	
Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile
					180				185					190	

Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr  
 195 200 205  
 Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys  
 210 215 220  
 Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys  
 225 230 235 240  
 Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp  
 245 250 255  
 Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp  
 260 265 270  
 Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe  
 275 280 285  
 Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr  
 290 295 300  
 Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp  
 305 310 315 320  
 Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys  
 325 330 335  
 Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met  
 340 345 350  
 Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn  
 355 360 365  
 Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp  
 370 375 380  
 Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr  
 385 390 395 400  
 His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp  
 405 410 415  
 Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala  
 420 425 430  
 Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu  
 435 440 445  
 Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser  
 450 455 460  
 Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr  
 465 470 475 480  
 Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr  
 485 490 495  
 Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Ala  
 500 505 510  
 Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser Ser  
 515 520 525  
 Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr  
 530 535 540  
 Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn  
 545 550 555 560  
 Lys Ala Lys Ser

<210> 16  
 <211> 565  
 <212> PRT  
 <213> Artificial Sequence

<220>  
<223> ORF0657nH

<400> 16

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu Thr  
 50 55 60  
 Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile  
 65 70 75 80  
 Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp  
 85 90 95  
 Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys  
 100 105 110  
 Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys  
 115 120 125  
 Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly  
 130 135 140  
 Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp  
 145 150 155 160  
 Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr  
 165 170 175  
 Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile  
 180 185 190  
 Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr  
 195 200 205  
 Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys  
 210 215 220  
 Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys  
 225 230 235 240  
 Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp  
 245 250 255  
 Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp  
 260 265 270  
 Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe  
 275 280 285  
 Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr  
 290 295 300  
 Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp  
 305 310 315 320  
 Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys  
 325 330 335  
 Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met  
 340 345 350  
 Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn  
 355 360 365  
 Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp  
 370 375 380  
 Ala Ile Val Arg Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr  
 385 390 395 400  
 His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp

405	410	415	
Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala			
420	425	430	
Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu			
435	440	445	
Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser			
450	455	460	
Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr			
465	470	475	480
Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr			
485	490	495	
Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr			
500	505	510	
Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser			
515	520	525	
Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn			
530	535	540	
Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu			
545	550	555	560
Asn Lys Ala Lys Ser			
565			

<210> 17  
 <211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 17			
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu			
1	5	10	15
Ala Leu Ala Ser Pro Thr Thr Thr Glu Lys Ala Pro Glu Thr Lys			
20	25	30	
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro			
35	40	45	
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro			
50	55	60	
Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr			
65	70	75	80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala			
85	90	95	
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe			
100	105	110	
Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser			
115	120	125	
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile			
130	135	140	
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr			
145	150	155	160
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val			
165	170	175	

Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Ile Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

<210> 18  
 <211> 565  
 <212> PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 18

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5				10						15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys
					20			25						30	
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
					35			40						45	
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr
				50			55			60					50
Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile
					65		70		75					80	
Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp
					85			90						95	
Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys
					100			105						110	
Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys
					115		120						125		115
Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly
					130		135					140		130	
Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp
					145		150		155					160	
Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr
					165			170					175		165
Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile
					180			185					190		180
Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr
					195			200			205				195
Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys
					210		215				220				210
Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys
					225		230		235					240	
Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp
					245			250					255		245
Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp
					260			265				270		260	
Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe
					275			280				285		275	
Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr
					290		295				300				290
Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp
					305		310		315					320	
Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys
					325			330					335		325
Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met
					340			345				350		340	
Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn
					355			360				365		355	
Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp
					370			375			380				370

Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr  
 385 390 395 400  
 His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp  
 405 410 415  
 Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala  
 420 425 430  
 Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu  
 435 440 445  
 Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Pro Leu Pro Ser  
 450 455 460  
 Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr  
 465 470 475 480  
 Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr  
 485 490 495  
 Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr  
 500 505 510  
 Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser  
 515 520 525  
 Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn  
 530 535 540  
 Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu  
 545 550 555 560  
 Asn Lys Ala Lys Ser  
 565

<210> 19  
 <211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 19

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Ala Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160

Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Arg Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

<211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 20  
 Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Ala Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160  
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365

Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

<210> 21  
 <211> 576  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 21

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 Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala  
 20 25 30  
 Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys  
 35 40 45  
 Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys  
 50 55 60  
 Ala Val Lys Glu Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro  
 65 70 75 80  
 Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu  
 85 90 95  
 Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala  
 100 105 110  
 Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr  
 115 120 125  
 Gln Gln Phe Tyr His Tyr Ala Gly Ser Val Lys Pro Ala Arg Val Ile  
 130 135 140

Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln  
 145 150 155 160  
 Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile  
 165 170 175  
 Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe  
 180 185 190  
 Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His  
 195 200 205  
 Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala  
 210 215 220  
 Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr  
 225 230 235 240  
 Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu  
 245 250 255  
 Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys  
 260 265 270  
 Leu Lys Ala Glu Tyr Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu  
 275 280 285  
 Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro  
 290 295 300  
 Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr  
 305 310 315 320  
 Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His  
 325 330 335  
 Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu  
 340 345 350  
 Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg  
 355 360 365  
 Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile  
 370 375 380  
 Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val  
 385 390 395 400  
 His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val  
 405 410 415  
 Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys  
 420 425 430  
 Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro  
 435 440 445  
 Ser Lys Pro Thr Thr Pro Val Glu Lys Glu Ser Gln Lys Gln Asp  
 450 455 460  
 Ser Gln Lys Asp Asp Asn Lys Gln Ser Pro Gly Val Glu Lys Glu Asn  
 465 470 475 480  
 Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro  
 485 490 495  
 Ala Lys Ala Glu Val Glu Ser Ser Thr Thr Pro Thr Lys Val Val  
 500 505 510  
 Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr  
 515 520 525  
 Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp  
 530 535 540  
 Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His  
 545 550 555 560  
 Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 565 570 575

<210> 22  
 <211> 576  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

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 Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys  
 35 40 45  
 Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys  
 50 55 60  
 Ala Val Lys Glu Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro  
 65 70 75 80  
 Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu  
 85 90 95  
 Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala  
 100 105 110  
 Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr  
 115 120 125  
 Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile  
 130 135 140  
 Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln  
 145 150 155 160  
 Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile  
 165 170 175  
 Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe  
 180 185 190  
 Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His  
 195 200 205  
 Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala  
 210 215 220  
 Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr  
 225 230 235 240  
 Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu  
 245 250 255  
 Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys  
 260 265 270  
 Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu  
 275 280 285  
 Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro  
 290 295 300  
 Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr  
 305 310 315 320  
 Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His  
 325 330 335  
 Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu  
 340 345 350

Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg  
 355 360 365  
 Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile  
 370 375 380  
 Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val  
 385 390 395 400  
 His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val  
 405 410 415  
 Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys  
 420 425 430  
 Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro  
 435 440 445  
 Ser Lys Pro Thr Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp  
 450 455 460  
 Ser Gln Lys Asp Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn  
 465 470 475 480  
 Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro  
 485 490 495  
 Ala Lys Ala Glu Val Glu Ser Ser Thr Thr Pro Thr Lys Val Val  
 500 505 510  
 Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr  
 515 520 525  
 Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp  
 530 535 540  
 Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His  
 545 550 555 560  
 Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 565 570 575

<210> 23  
 <211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 23

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
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Ala	Val	Ala	Ser	Pro	Ser	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys
														30	
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
														45	
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
														50	
														55	60
Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Thr	Lys	Ala	Asp	Asn	Asn	Thr
														65	70
														75	80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
														85	90
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
														100	105
Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
														115	120
														125	

Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160  
 Glu Gly Asn Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Gly  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ser Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Ala Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Thr Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Pro Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Ser Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Thr Lys Pro Ala Lys Ala Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Glu Thr Thr Ile Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Glu Asn Asn Lys Asn  
 545 550 555 560

Thr Gln Glu Asn Lys Ala Lys Ser  
565

<210> 24  
<211> 568  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> ORF0657nH

<400> 24  
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
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Ala Val Ala Ser Pro Ser Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys  
20 25 30  
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
35 40 45  
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
50 55 60  
Lys Glu Thr Lys Glu Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr  
65 70 75 80  
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
85 90 95  
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
100 105 110  
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser  
115 120 125  
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
130 135 140  
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
145 150 155 160  
Glu Gly Asn Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
165 170 175  
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
180 185 190  
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
195 200 205  
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
210 215 220  
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ser Pro  
225 230 235 240  
Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
245 250 255  
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
260 265 270  
Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
275 280 285  
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
290 295 300  
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
305 310 315 320  
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
325 330 335

Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Ala Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Thr Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Pro Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Ser Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Ala Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Glu Thr Thr Ile Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Glu Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

<210> 25  
 <211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 25  
 Ala Glu Glu Thr Gly Gly Thr Ile Thr Glu Thr Gln Pro Lys Thr Glu  
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 Ala Val Ala Ser Pro Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Ala Ala Pro  
 35 40 45  
 Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Asn Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ser Asp Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Glu Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110

Glu Met Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160  
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Glu Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Ala Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Thr Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Ala Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Ser Pro Ser Val Glu Lys Glu Ile Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Ala Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Ser Ala Ser Ser Glu Thr Thr Lys Gly Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Asn Ala Pro Leu Gln Lys Ala Asn  
 530 535 540

Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn
545															560
Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser								
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<210> 26  
 <211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 26															
Ala	Glu	Glu	Thr	Gly	Gly	Thr	Ile	Thr	Glu	Thr	Gln	Pro	Lys	Thr	Glu
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Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys
															30
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Val	Ala	Pro
															45
Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
															50
Asn	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ser	Asp	Asn	Asn	Thr
65															80
Tyr	Pro	Ile	Leu	Asn	Glu	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
															95
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
															100
Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
															110
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
															115
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145															125
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
															130
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
															135
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
															140
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
															145
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225															150
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
															155
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
															160
Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
															165
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
290															170
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305															175
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Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
				325					330				335		
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
				340			345						350		
Asp	Phe	Met	Val	Glu	Gly	Glu	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
				355			360						365		
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
				370			375						380		
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
				385		390				395			400		
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
				405				410					415		
Asn	Ala	Asp	Lys	Ser	Asn	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	
				420			425						430		
Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Thr	Ala	Pro	Val
				435			440						445		
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln
				450			455						460		
Ser	Pro	Ser	Val	Glu	Lys	Glu	Ile	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys
				465			470			475			480		
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser
				485				490					495		
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Ala	Thr	Gln	Asn	Val	Ala	Lys
				500				505					510		
Pro	Thr	Ser	Ala	Ser	Ser	Glu	Thr	Thr	Lys	Gly	Val	Val	Gln	Thr	Ser
				515				520					525		
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Asn	Ala	Pro	Leu	Gln	Lys	Ala	Asn
				530			535					540			
Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn
				545			550			555			560		
Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser								
				565											

<210> 27  
 <211> 570  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

Met	Gly	Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys
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Thr	Glu	Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu
				20			25						30		
Thr	Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu
				35			40						45		
Ala	Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys
				50			55					60			
Ala	Pro	Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn
				65			70			75			80		
Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn
				85				90					95		

Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile  
 100 105 110  
 Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr  
 115 120 125  
 Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro  
 130 135 140  
 Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu  
 145 150 155 160  
 Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp  
 165 170 175  
 Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr  
 180 185 190  
 Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu  
 195 200 205  
 Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser  
 210 215 220  
 Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu  
 225 230 235 240  
 Ala Pro Tyr Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu  
 245 250 255  
 Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys  
 260 265 270  
 Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser  
 275 280 285  
 Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr  
 290 295 300  
 Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn  
 305 310 315 320  
 Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met  
 325 330 335  
 Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr  
 340 345 350  
 Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys  
 355 360 365  
 Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly  
 370 375 380  
 Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp  
 385 390 395 400  
 Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr  
 405 410 415  
 Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser  
 420 425 430  
 Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser  
 435 440 445  
 Pro Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn  
 450 455 460  
 Lys Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser  
 465 470 475 480  
 Gly Lys Gly Val Thr Leu Ala Thr Lys Pro Thr Lys Gly Glu Val Glu  
 485 490 495  
 Ser Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val  
 500 505 510  
 Ala Lys Pro Thr Thr Gly Ser Ser Lys Thr Thr Lys Asp Val Val Gln  
 515 520 525

Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys
530						535						540			
Ala	Asn	Ile	Lys	His	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn
545						550					555				560
Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser						
						565					570				

<210> 28  
 <211> 654  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SEQ ID NO: 2 modified to contain a glycine after  
 the amino terminus methionine and a carboxyl  
 His-Tag

<400> 28																
Met	Gly	Asn	Lys	Gln	Gln	Lys	Glu	Phe	Lys	Ser	Phe	Tyr	Ser	Ile	Arg	
1							5			10				15		
Lys	Ser	Ser	Leu	Gly	Val	Ala	Ser	Val	Ala	Ile	Ser	Thr	Leu	Leu	Leu	
								20		25				30		
Leu	Met	Ser	Asn	Gly	Glu	Ala	Gln	Ala	Ala	Ala	Glu	Glu	Thr	Gly	Gly	
							35		40			45				
Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	Ala	Val	Ala	Ser	Pro	Thr	
							50		55			60				
Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys	Pro	Val	Ala	Asn	Ala	Val	
							65		70		75			80		
Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	Thr	Ser	Glu	Thr	Lys	Glu	
							85			90			95			
Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr	Lys	Glu	Val	
							100		105			110				
Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	
							115		120			125				
Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	
							130		135			140				
Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	
							145		150		155			160		
Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	
							165			170			175			
Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	
							180		185			190				
Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	
							195		200			205				
Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	
							210		215			220				
Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	
							225		230		235			240		
Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	
							245			250			255			
Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	
							260		265			270				
Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	
							275		280			285				

Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro  
 290 295 300  
 Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys  
 305 310 315 320  
 Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val  
 325 330 335  
 Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val  
 340 345 350  
 Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val  
 355 360 365  
 Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val  
 370 375 380  
 Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly  
 385 390 395 400  
 Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr  
 405 410 415  
 Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val  
 420 425 430  
 Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg  
 435 440 445  
 Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn  
 450 455 460  
 Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala  
 465 470 475 480  
 Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys  
 485 490 495  
 Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys  
 500 505 510  
 Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr  
 515 520 525  
 Lys Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys  
 530 535 540  
 Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser  
 545 550 555 560  
 Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala  
 565 570 575  
 Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp  
 580 585 590  
 Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala  
 595 600 605  
 Lys Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu  
 610 615 620  
 Pro Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu  
 625 630 635 640  
 Pro Arg Lys Arg Lys Asn Leu Glu His His His His His His His  
 645 650

<210> 29  
 <211> 1962  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Full length ORF0657n + Carboxyl His-Tag

&lt;400&gt; 29

atgaacaaac agcaaaaaga atttaaatca ttttattcaa ttagaaagtc atcaactaggc 60  
 gttgcattctg tagcaatttag tacactttt ttattaaatgt caaatggcga agcacaagca 120  
 gcagctgaag aaacagggtgg tacaatataca gaagcacaac caaaaactga agcagttgca 180  
 agtccaacaa caacatctga aaaagctcca gaaactaaac cagtagctaa tgctgtctca 240  
 gtatctaata aagaagttga ggcccctact tctgaaacaa aagaagctaa agaagttaaa 300  
 gaagttaaag cccctaagga aacaaaagaa gttaaaccag cagcaaaagc cactaacaat 360  
 acatatccta ttttgaatca ggaacttaga gaagcgatta aaaaccctgc aataaaagac 420  
 aaagatcata gcgacccaaa ctctcgctca attgattttg aaatgaaaaa gaaagatgga 480  
 actcaacagt tttatcatta tgcaagttct gttaaacctg cttagagttat tttcaactgat 540  
 tcaaaaaccag aaattgaatt aggattacaa tcaggtcaat tttggagaaa atttgaagtt 600  
 tatgaagggtg aaaaaaagtt gccaattaaa ttagtacat acgatactgt taaagattat 660  
 gcttacattc gcttctctgt atcaaacgga acaaagctg ttaaaattgt tagttcaaca 720  
 cacttcaata acaaagaaga aaaatacat tacacattaa tggatttcgc acaaccaatt 780  
 tataacagtg cagataaatt caaaactgaa gaagattata aagctgaaaa attattagcg 840  
 ccataaaaaa aagcgaaaac actagaaaga caagtttatg aattaaataa aattcaagat 900  
 aaacttcctg aaaaattaaa ggctgagtag aagaagaaat tagaggatac aaagaaagct 960  
 ttagatgagc aagtgaaatc agctattact gaattccaaa atgtacaacc aacaatgaa 1020  
 aaaaatgactg atttacaaga tacaatataat gttgtttatg aaagtgttga gaataacgaa 1080  
 tctatgatgg atactttgt taaacaccct attaaaacag gtatgcttaa cggcaaaaaa 1140  
 tatatggtca tggaaactac taatgacat tactggaaag atttcatggt tgaaggtcaa 1200  
 cgtgttagaa ctataagcaa agatgctaaa aataatacta gaacaattat tttccatata 1260  
 gttgaaggta aaactctata tgatgctatc gttaaagttc acgtaaaaac gattgattat 1320  
 gatggacaat accatgtcag aatcggtat aaagaagcat ttacaaaagc caataccat 1380  
 aaatctaaca aaaaagaaca acaagataac tcagctaaaga aggaagctac tccagctacg 1440  
 cctagcaaacc acacaccatc acctgttcaa aaagaatcac aaaaacaaga cagccaaaaa 1500  
 gatgacaata aacaattacc aagtgttcaa aaagaaaaatg acgcatctag ttagtcaggt 1560  
 aaagacaaaaa cgcctgctac aaaaccaact aaaggtgaag tagaatcaag tagtacaact 1620  
 ccaactaagg tagtatctac gactctaaat gttcaaaac caacaactgc ttcatcaaaa 1680  
 acaacaaaaa atgttgcata aacttcagca ggttctagcg aagcaaaaga tagtgctcca 1740  
 ttacaaaaaag caaacattaa aaacacaaat gatggacaca ctcaaagcca aaacaataaa 1800  
 aatacacaag aaaataaaagc aaaatcatta ccacaaactg gtgaagaatc aaataaaagat 1860  
 atgacattac catatggc attattagct ttaagtagca tcgttgcatt cgtattacat 1920  
 agaaaacgtaa aaaacctcgaa gcaccaccac caccaccact ga 1962

&lt;210&gt; 30

&lt;211&gt; 1737

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH + Carboxyl His-Tag

&lt;400&gt; 30

atgaacgctg aagaaacagg tggtacaaat acagaagcac aaccaaaaaac tgaagcagtt 60  
 gcaagtccaa caacaacatc taaaaaagct ccagaaacta aaccagtagc taatgctgtc 120  
 tcagttatcta ataaagaagt tgaggccct acttctgaaa caaaaagaagc taaagaagtt 180  
 aaagaagtt aagccctaa ggaaacaaaaa gaagttaaac cagcagcaaa agccactaac 240  
 aatacatatc ctatggaa tcaggaacctt agagaagcga taaaaaacc tgcataaaaa 300  
 gacaaagatc atagcgcacc aaactctctgt ccaatttgatt ttgaaatgaa aaagaaaagat 360  
 ggaactcaac agtttatca ttatgcaagt tctgttaaac ctgcttagagt tattttcact 420  
 gattcaaaaac cagaaattga attaggatta caatcaggc aattttggag aaaatttggaa 480  
 gtttatgaaat gtcacaaaaa gttgccaattt aaatttagtat catabgatac tttttaaagat 540  
 tatgcttaca ttgcgttctc tttatcaac ggaacaaaaat ttgttagttca 600

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acacacttca ataacaaaga agaaaaatac gattacacat taatggaatt cgcacaaacca 660
atttataaca gtgcagataa attcaaaaact gaagaagatt ataaagctga aaaatttata 720
gcgcctatca aaaaagcgaa aacactagaa agacaagttt atgaattaaa taaaattcaa 780
gataaaacttc ctgaaaaatt aaaggctgag tacaagaaga aatttagagga tacaagaaa 840
gttttagatg agcaagtgaa atcagctatt actgaattcc aaaatgtaca accaacaat 900
gaaaaaatga ctgatttaca agatacaaaa tatgttgtt atgaaagtgt tgagaataac 960
gaatctatga tggatactt tggtaaacac cctattaaa caggtatgct taacggcaaa 1020
aaatatatgg tcatggaaac tactaatgac gattactgga aagatttcat ggttgaagg 1080
caacgtgtt gaactataag caaagatgct aaaaataata ctagaacaat tattttccca 1140
tatgttgaag gtaaaactct atatgtgct atcgtaaag ttcacgtaaa aacgattgat 1200
tatgtatggac aataccatgt cagaatcggt gataaagaag catttacaaa agccaatacc 1260
gataaatcta acaaaaaaga acaacaagat aactcagcta agaaggaagc tactccagct 1320
acgcctagca aaccaacacc atcacctggt gaaaaagaat cacaaaaaca agacagccaa 1380
aaagatgaca ataaacaatt accaagtgtt gaaaaagaaa atgacgcac tagtgagtca 1440
ggtaaagaca aaacgcttc tacaaaacca actaaagggtg aagtagaatc aagtagtaca 1500
actccaacta aggtagtatc tacgactcaa aatgttgcaa aaccaacaac tgcttcatca 1560
aaaacaacaa aagatgttgt tcaaacttca gcaggttcta gcgaagcaaa agatagtgt 1620
ccattacaaa aagcaaacat taaaaacaca aatgatggac acactcaaag ccaaaacaat 1680
aaaaatacac aagaaaataa agcaaaatca ctgcagcacc accaccacca ccactga 1737

```

<210> 31  
<211> 1941  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Encodes SEQ ID NO: 28 without a carboxyl His-Tag  
and is codon optimized for yeast expression

<400> 31

```

atgggttaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtttcccttg 60
ggtgttgcctt ctgtcgctat ctccacctt ttgttggta tgcgttacgg tgaagctcaa 120
gctgctgtgt aagaaaactgg tggtaccaac actgaagctc aaccaaaagac cgaagctgtc 180
gttcccccac ccactacctc tggaaaggct ccagaaacta agccagttgc taacgctgtc 240
tccgtttctt acaaggaagt cgaagctcca acctccgaaa ctaaggaagc taaggaagg 300
aaggaagtca aggctccaaa gggaaactaag gaagtcaagc cagctgctaa ggctaccaac 360
aacacttacc caattttgaa ccaagaattt agagaagcta ttaagaaccc agctatcaag 420
gacaaggacc actccgctcc aaactctaga ccaatcgact tcgaaatgaa gaagaaggac 480
ggtacccaaac aatttacca ctacgcgtcc tctgtcaagc cagctagagt tattttcacc 540
gactctaagc cagaaatcga attgggtttt caatccggc aattctggag aaagttcgaa 600
gtctacgaag gtgacaagaa gttgccaatt aagttggttt cctacgacac cgtcaaggac 660
tacgcttaca tcagattctc cgtttcttaac ggtactaagg ctgtcaagat tgcgttcc 720
acccacttca acaacaagga agaaaaagtac gactacactt tgcgttaccc cgctcaacca 780
atttacaact ctgctgacaa gttcaagacc gaagaagact acaaggctga aaagttgtt 840
gctccataca agaaggctaa gactttggaa agacaagttt acgaattgaa caagatccaa 900
gacaagggtc cagaaaagtt gaaggctgaa tacaagaaga agttggaaaga caccacaaag 960
gtttggacg aacaagtcaa gtccgctatc accgaattcc aaaacgttca accaactaac 1020
gaaaagatga ctgacttgca agacactaag tacgtcgct acgaattccgt cgaaaacaac 1080
gaatccatga tggacacctt cgttaagcac ccaattaaga ctggatgtt gaacggtaag 1140
aagtacatgg tcatgaaac cactaacgac gactactgga aggacttcat ggttgaagg 1200
caaagagtca gaaccatctc caaggacgct aagaacaaca ctggatgtt gaacggtaag 1260
tacgttgaag gtaagacttt gtacgacgct atcgtaagg ttcacgtcaa gactattgac 1320
tacgacggtc aataccacgt tagaattgtt gacaaggaag ctggatgtt gaacggtaag 1380
gacaagtcca acaagaagga acaacaagac aactctgcta agaaggaagc taccacca 1440
accccatcta agccaaacccc atctccagtt gaaaaggaat ctggatgtt gaacggtaag 1500

```

```

aaggacgaca acaagcaatt gccatccgtc gaaaaggaaa acgacgcgtc ttctgaatcc 1560
ggttaaggaca agactccagc taccaagcca actaagggtg aagttgaatc ttccctctact 1620
actccaacca aggttgtctc cactacccaa aacgtcgcta agccaactac cgcttcttcc 1680
aagactacca aggacgttgt ccaaacttct gctgggttctt ctgaagctaa ggactctgct 1740
ccattgcaaa aggctaacat caagaacaccc aacgacggtc acacccaatc ccaaaaacaac 1800
aagaacactc aagaaaacaa ggctaagttt ttgccacaaa ccggtgaaaga atccaacaag 1860
gacatgacct tgccattgtat ggctttgtt gctttgttcc ccatcggtgc ttctgtctg 1920
ccaagaaaaga gaaagaacta a 1941

```

```

<210> 32
<211> 1710
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Encodes SEQ ID NO: 3 and is codon optimized for
      yeast expression

```

```

<400> 32
atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tcccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagcttata agaaccacgc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag cttagagttt ttccaccgac 420
tctaagccag aaatcgaatt gggtttgc当地 tccggtaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaattaag ttgggttctt acgacaccgt caaggactac 540
gcttacatca gatttccgt ttctaaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacacttga tggaaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtctgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acacccctcgtaa agtgcacccatc attaagactg gtatgtgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgcacgc tactggagg acttcatggt tgaaggtcaa 1080
agagtcaagaa ccatctccaa ggacgctaa aacaacacta gaaccattat ctccccatc 1140
gttgaaggta agactttgtt cgcgtctacgt gtcaagggtt acgtcaagac tattgactac 1200
gacggtaat accacgttag aatttggtaa aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaaca agaagaaca acaagacaac tctgtctaa aaggaagctac cccagctacc 1320
ccatctaagc caacccatc tccagttgaa aaggaatctc aaaagcaaga ctccccaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aagaaaaacg acgcgtcttc tgaatccggt 1440
aaggacaaga ctccagctac caagccaaact aagggtgaag ttgaatctt ctctactact 1500
ccatccaaagg ttgttccac tacccaaaac gtcgctaaacg caactaccgc ttcttccaa 1560
actaccaagg acgttgttccaa aacttctgtt ggttcctctg aagctaagga ctctgtctca 1620
ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtctttaa 1710

```

```

<210> 33
<211> 1341
<212> DNA
<213> Artificial Sequence

```

```

<220>

```

<223> Encodes SEQ ID NO: 1 and is codon optimized for yeast expression

<400> 33

```

atggctgaag aaactggtgg taccacact gaagctcaac caaagaccga agctgtcgct 60
tcccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacgc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgctcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaaatt gggtttgc当地 tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaattaag ttggtttccct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggg actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaagaaga aaagtacgac tacacttga tggaaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggtggct 720
ccatacaaga aggctaaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaat ac aagaagaagt tggaaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgc当地 aactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acacccctgt taagcacccca attaagactg gtatgtgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggagg acttcatggg tgaaggctcaa 1080
agagtcaaggaa ccatctccaa ggacgctaa ag aacaacacta gaaccattat cttccctata 1140
gttgaaggtt agactttgtt cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200
gacggtaat accacgttag aattgttgc当地 aaggaaagctt tcaccaaggc taacaccgac 1260
aagtccaaaca agaagaaca acaagacaac tctgctaa aggaagctac cccagctacc 1320
ccatctaagc caacccata a 1341

```

<210> 34

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus methionine and is codon optimized for yeast expression

<400> 34

```

atggctgaag aaactggtgg taccacact gaagctcaac caaagaccga agctgtcgct 60
tcccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacgc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgctcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaaatt gggtttgc当地 tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaattaag ttggtttccct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggg actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaagaaga aaagtacgac tacacttga tggaaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggtggct 720
ccatacaaga aggctaaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaat ac aagaagaagt tggaaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgc当地 cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960

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tccatgatgg acacccctcgtaaagcacccattaagactgtatgttgaacggtaagaag 1020  
 tacatggtca tggaaaccac taacgacgactacttggaggacttcatggttgaaggtaa 1080  
 agagtcagaa ccatctccaa ggacgctaagaacaacactagaaccattatcttccat 1140  
 gttgaaggta agacttgcgacgctatcgtcaagggttacgtcaagac tattgactac 1200  
 gacggtcaat accacgttag aattgttgcgaaaggagtttcaccaaggctaacaccgac 1260  
 aagtccaaaca agaaggaaaca acaagacaactctgcttaagaaggagctacc 1320  
 ccatctaagcaacccatctccagttgaaaagaatctcaaaagcaagaactccaaaag 1380  
 gacgacaaca agcaattgccatccgtcgaa aagaaaacg acgcgttctc tgaatccggt 1440  
 aagggtgtca ctttggctac caagccaaactaagggtgaagttgaatcttctctact 1500  
 ccaaccaagg ttgtctccac tacccaaaccgtcgcttaagcaactaccgg ttcttccaag 1560  
 actaccaagg acgttgtcca aacttctgct gttcctctgaagctaagga ctctgctcca 1620  
 ttgcaaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680  
 aacactcaag aaaacaaggcttaagttttaa 1710

<210> 35  
 <211> 1710  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Encodes SEQ ID NO: 7 containing an amino terminus  
 methionine and is codon optimized for yeast  
 expression

<400> 35  
 atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60  
 tcccccaacca ctacctctga aaaggctcca gaaactaagc cagttctaa cgctgtctcc 120  
 gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagtttaag 180  
 gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgcttaaggc taccaacaac 240  
 acttacccaa ttttgaacca agaattgaga gaagcttata agaaccacgatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aatgaagaa gaaggacggt 360  
 acccaacaat tctaccacta cgcgtcctct gtcaagccag cttaggttat tttcaccgac 420  
 tctaagccag aaatcgaatt gggtttgcgaa tccggtaat tctggagaaa gttcgaagtc 480  
 tacgaagggtg acaagaagtt gccaattaaat ttgtttctt acgacaccgt caaggactac 540  
 gtttacatca gatttccgt ttcttaacggt actaaggctg tcaagattgt ctcttccacc 600  
 cacttcaaca acaaggaaga aaagtacgac tacacttgcgaa tggaaattcgc tcaaccaatt 660  
 tacaactctg ctgacaaggaa caagaccgaa gaagactaca aggctgaaaa gttgttggt 720  
 ccatacaaga aggctaaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaaagacac caagaaggct 840  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgcaga aactaaggatcgtctacg aatccgtcga aaacaacgaa 960  
 tccatgatgg acacccctcgtaaagcacccattaagactgtatgttgaacggtaagaag 1020  
 tacatggtca tggaaaccac taacgacgactacttggaggacttcatggttgaaggtaa 1080  
 agagtcagaa ccatctccaa ggacgctaaga aacaacactagaaccattatcttccat 1140  
 gttgaaggta agacttgcgacgctatcgtcaagggttacgtcaagac tattgactac 1200  
 gacggtcaat accacgttag aattgttgcgaaaggagtttcaccaaggctaacaccgac 1260  
 aagtccaaaca agaaggaaaca acaagacaactctgcttaagaaggagctacc 1320  
 ccatctaagcaacccatctccagttgaaggaaatctcaaaagcaagaactccaaaag 1380  
 gacgacaaca agcaattgccatccgtcgaa aagaaaacg acgcgttctc tgaatccggt 1440  
 aagggtgtca ctttggctac caagccaaactaagggtgaagttgaatcttctctact 1500  
 ccaaccaagg ttgtctccac tacccaaaccgtcgcttaagcaactaccgg ttcttccaag 1560  
 actaccaagg acgttgtcca aacttctgct gttcctctgaagctaagga ctctgctcca 1620  
 ttgcaaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680  
 aacactcaag aaaacaaggcttaagttttaa 1710

<210> 36  
 <211> 1710  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Encodes SEQ ID NO: 7 containing an amino terminus  
 methionine and is codon optimized for yeast  
 expression

<400> 36  
 atggctgaag aaactggtgg taccacact gaagctcaac caaagaccga agctgtcgct 60  
 tcccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120  
 gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180  
 gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccacaaac 240  
 acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacgc tatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacgt 360  
 acccaacaat tctaccacta cgcgtcctct gtcaagccag cttagagttat tttcaccgac 420  
 tctaagccag aaatcgaatt gggtttgc当地 tccggtaat tctggagaaa gttcgaagtc 480  
 tacgaaggtg acaagaagtt gccaattaag ttgtttcct acgacaccgt caaggactac 540  
 gcttacatca gatttccgt ttctaacggc actaaggctg tcaagattgt ctcttccacc 600  
 cacttcaaca acaaggaaga aaagtacgac tacacttga tggaaattcgc tcaaccaatt 660  
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720  
 ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaaagacac caagaaggt 840  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgcaaga cactaagtac gtgcgtctacg aatccgtcga aaacaacgaa 960  
 tccatgatgg acacccctcgtaa agtgcacca attaagactg gtatgttgcg cggtaagaag 1020  
 tacatggta tggaaaccac taacgcacac tactggagg acttcatggc tgaaggtcaa 1080  
 agagtcaagaa ccatctccaa ggacgctaa aacaacacta gaaccattat ctccccatc 1140  
 gttgaaggta agactttgtt cgcgcgtatc gtcaagggttc acgtcaagac tattgactac 1200  
 gacggtaat accacgttag aattgttgcg aaggaaagctt tcaccaaggc taacaccgac 1260  
 aagtccaaaca agaaggaaca acaagacaaac tctgctaaga aggaagctac cccagctacc 1320  
 ccatctaagc caaccccatc tccagttgaa aagaatctc aaaagcaaga ctccccaaag 1380  
 gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccgt 1440  
 aagggtgtt ctttggctac caagccaaact aagggtgaag ttgaatcttc ctctactact 1500  
 ccaaccaagg ttgttccac taccacaaac gtgcctaagc caactaccgg ttcttccaaag 1560  
 actaccaagg acgttgtcca aacttctgct gtttctctg aagctaagga ctctgctcca 1620  
 ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680  
 aacactcaag aaaacaaggc taagtcttaa 1710

<210> 37  
 <211> 1710  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Encodes SEQ ID NO: 7 containing an amino terminus  
 methionine and is codon optimized for yeast  
 expression

<400> 37  
 atggctgaag aaactggtgg taccacact gaagctcaac caaagaccga agctgtcgct 60  
 tcccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120  
 gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180

gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaaggc taccaacaac 240  
 acttacccaa ttttgaacca agaattgaga gaagctatta agaaccgc tatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360  
 acccaacaat tctaccacta cgcgtcctct gtcaagccag cttaggttat tttcaccgac 420  
 tctaagccag aaatcgaatt gggtttgc当地 tccggtaat tctggagaaa gttcgaagtc 480  
 tacgaaggtg acaagaagtt gccaattaag ttgtttcct acgacaccgt caaggactac 540  
 gcttacatca gatttccgt ttctaaacggt actaaggctg tcaagattgt ctcttccacc 600  
 cacttcaaca acaaggaaga aaagtacgac tacacttga tggaaatcgc tcaaccaatt 660  
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720  
 ccataacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagtgaa ggctgaatac aagaagaagt tggaaagacac caagaaggct 840  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgc当地 aactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960  
 tccatgatgg acacccctgt taagcacccca attaagactg gtatgttgc当地 cggttaagaag 1020  
 tacatggtca tggaaaccac taacgacgac tacttggagg acttcatggt tgaaggtcaa 1080  
 agagtcaagaa ccattccaa ggacgctaa aacaacacta gaaccattat ctcccatac 1140  
 gttgaaggta agactttgtt ctagctatcgt gtcaagggtt acgtcaagac tattgactac 1200  
 gacggtaat accacgttag aatttggac aagaagctt tcaccaaggc taacaccgac 1260  
 aagtccaaaca agaaggaaca acaagacaac tctgctaa aagaagctac cccagctacc 1320  
 ccattctaaaggc caaccccatc tccagttgaa aagaatctc aaaagcaaga ctcccaaaag 1380  
 gacgacaaca agcaatttgc当地 atccgtc当地 aagaaaaacg acgcgtctt tgaatccggt 1440  
 aagggcgtt当地 ctttggctac caagccact aagggtgaag ttgaatctt ctctactact 1500  
 ccaaccaagg ttgttccac taccctaaac gtcgctaaac caactaccgg ttcttccaaag 1560  
 actaccaagg acgttgc当地 aacttctgtt gttcctctg aagctaagga ctctgctcc 1620  
 ttgcaaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaaatccca aaacaacaag 1680  
 aacactcaag aaaacaaggc taagtctt当地 1710

<210> 38

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus methionine and is codon optimized for yeast expression

<400> 38

atggctgaag aaacttgggg taccacactt gaagctcaac caaagaccga agctgtcgct 60  
 tcccccaacca ctacctctga aaaggctcca gaaactaagc cagttgtctaa cgctgtctcc 120  
 gtttctaaaca aggaagtc当地 agcttcaacc tccggaaacta aggaagctaa ggaagttaag 180  
 gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaaggc taccacaaac 240  
 acttacccaa ttttgaacca agaattgaga gaagctatta agaaccgc tatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360  
 acccaacaat tctaccacta cgcgtcctct gtcaagccag cttaggttat tttcaccgac 420  
 tctaagccag aaatcgaattt gggtttgc当地 tccggtaat tctggagaaa gttcgaagtc 480  
 tacgaaggtg acaagaagtt gccaattaag ttgtttcct acgacaccgt caaggactac 540  
 gcttacatca gatttccgt ttctaaacggt actaaggctg tcaagattgt ctcttccacc 600  
 cacttcaaca acaaggaaga aaagtacgac tacacttga tggaaatcgc tcaaccaatt 660  
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720  
 ccataacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagtgaa ggctgaatac aagaagaagt tggaaagacac caagaaggct 840  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgc当地 aactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960  
 tccatgatgg acacccctgt taagcacccca attaagactg gtatgttgc当地 cggttaagaag 1020

tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggtcaa 1080  
 agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttccatac 1140  
 gttgaaggtta agactttgtt ctagcgtatac gtcaagggtt acgtcaagac tattgactac 1200  
 gacggtcaat accacgttag aattgttgc aaggaagctt tcaccaaggc taacaccgac 1260  
 aagtccaaaca agaaggaaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320  
 ccatctaagc caaccccatc tccagttgaa aagaatctc aaaagcaaga ctcccaaaag 1380  
 gacgacaaca agcaattgcc atccgtcgaa aagaaaacg acgcgtcttc tgaatccgt 1440  
 aagggtgtca ctttagctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500  
 ccaaccaagg ttgtctccac tacccaaacc gtcgctaagc caactaccgg ttcttccaag 1560  
 actaccaagg acgttgc aacttctgct gttcctctg aagctaagga ctctgctcca 1620  
 ttgaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680  
 aacactcaag aaaacaaggc taagtctaa 1710

<210> 39

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus  
methionine and is codon optimized for yeast  
expression

<400> 39

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60  
 tcccaacca ctacccctga aaaggctcca gaaactaago cagttctaa cgctgtctcc 120  
 gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaaag 180  
 gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240  
 acttacccaa ttttgaacca agaattgaga gaagctatta agaaccaccg tatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360  
 acccaacaaat tctaccacta cgcgtccctc gtcaagccag cttaggttat ttccaccgac 420  
 tctaagccag aaatcgaatt gggtttgc aa tccggtaat tctggagaaa gttcaagtc 480  
 tacgaagggtg acaagaagtt gccaattaag ttggttctt acgacaccgt caaggactac 540  
 gcttacatca gatttccgt ttctaacggg actaaggctg tcaagattgt ctcttccacc 600  
 cacttcaaca acaaggaaga aaagtacgac tacacttga tggattcgc tcaaccaatt 660  
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720  
 ccatacaaga aggctaagac ttggaaaga caagtttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggagacac caagaaggct 840  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgc aactaagtac gtctactcg aatccgtcg aaacaacgaa 960  
 tccatgatgg acacccctgt taagcacca attaagactg gtatgtgaa cggtaagaag 1020  
 tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggtcaa 1080  
 agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttccatac 1140  
 gttgaaggtta agactttgtt ctagcgtatac gtcaagggtt acgtcaagac tattgactac 1200  
 gacggtcaat accacgttag aattgttgc aaggaagctt tcaccaaggc taacaccgac 1260  
 aagtccaaaca agaaggaaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320  
 ccatctaagc caaccccatc tccagttgaa aagaatctc aaaagcaaga ctcccaaaag 1380  
 gacgacaaca agcaattgcc atccgtcgaa aagaaaacg acgcgtcttc tgaatccgt 1440  
 aagggtgtca cttggctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500  
 ccaaccaagg ttgtctccac tacccaaacc gtcgctaagc caactaccgg ctcttccaag 1560  
 actaccaagg acgttgc aacttctgct gttcctctg aagctaagga ctctgctcca 1620  
 ttgaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680  
 aacactcaag aaaacaaggc taagtctaa 1710

<210> 40

<211> 1710  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Encodes SEQ ID NO: 7 containing an amino terminus  
     methionine and is codon optimized for yeast  
     expression  
  
 <400> 40

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60  
 tcccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120  
 gtttctaaca aggaagtcga agctccaacc tccgaaaacta aggaagctaa ggaagttaag 180  
 gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240  
 acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacgc tatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aatgaagaa gaaggacggt 360  
 acccaacaat tctaccacta cgcgtcctct gtcaagccag cttagagttat tttcaccgac 420  
 tctaagccag aaatcgaatt gggtttgc当地 tccggtaat tctggagaaa gttcgaagtc 480  
 tacgaaggta acaagaagtt gccaattaaag ttggtttcct acgacaccgt caaggactac 540  
 gcttacatca gatttccgt ttctaacggc actaaggctg tcaagattgt ctcttccacc 600  
 cacttcaaca acaaggaaga aaagtacgac tacacttga tggaaattcgc tcaaccaatt 660  
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720  
 ccatacaaga aggctaagac ttggaaaga caagtttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaaagacac caagaaggct 840  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgc当地 cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960  
 tccatgatgg acacccctcgtaa agcaccacca attaagactg gtatgttcaa cggtaagaag 1020  
 tacatggtca tggaaaccac taacgacgac tactggagg acttcatggc tgaaggtcaa 1080  
 agagtcagaa ccatctccaa ggacgctaaag aacaacacta gaaccattat cttccatata 1140  
 gttgaaggta agactttgtc cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200  
 gacggtaat accacgttag aattgttgc当地 aaggaagctt tcaccaaggc taacaccgac 1260  
 aagtccaaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320  
 ccatctaaacg caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctccccaaaag 1380  
 gacgacaaca agcaattgcc atccgtcgaa aagggaaacg acgcgtcttc tgaatccggt 1440  
 aagggtgtta cttagctac caagccact aagggtgaag ttgaatctt ctctactact 1500  
 ccaaccaagg ttgtctccac tacccaaaac gtcgctaaagc caactaccgg ttcttccaaag 1560  
 actaccaagg acgttgc当地 aacttctgct ggttctctg aagctaagga ctctgctcca 1620  
 ttgcaaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680  
 aacactcaag aaaacaaggc taagtcttaa 1710

<210> 41  
 <211> 1710  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Encodes SEQ ID NO: 7 containing an amino terminus  
     methionine and is codon optimized for yeast  
     expression  
  
 <400> 41

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60  
 tcccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120  
 gtttctaaca aggaagtcga agctccaacc tccgaaaacta aggaagctaa ggaagttaag 180  
 gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240

acttacccaa ttttgaacca agaattgaga gaagctatta agaaccaggc tatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacgg 360  
 acccaacaat tctaccacta cgcgtccctc gtcaagccag ctagagttat tttcaccgac 420  
 tctaagccag aaatcgaatt gggtttgc aa tccggtaat tctggagaaa gttcgaagtc 480  
 tacgaagggtg acaagaagtt gccaattaag ttggtttctc acgacaccgt caaggactac 540  
 gcttacatca gatttccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600  
 cacttcaaca acaagaaga aaagtacgac tacacttga tggaaatcgc tcaaccaatt 660  
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttgct 720  
 ccatacaaga aggctaagac tttggaaaga caagttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaaagacac caagaaggct 840  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgcaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960  
 tccatgatgg acacccgtt taagcacccca attaagactg gtatgtgaa cggtaagaag 1020  
 tacatggtca tggaaaccac taacgacgac tactggagg acttcatggt tgaaggtcaa 1080  
 agagtccagaa ccatctccaa ggacgctaa aacaacacta gaaccattat cttccatata 1140  
 gttgaaggta agactttgt a c g c g c t a t c g t a a g t t a c t a c 1200  
 gacggtaat accacgttag aattttgtac aagaagctt tcaccaaggc taacaccgac 1260  
 aagtccaaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320  
 ccatctaagc caacccatc tccagttgaa aagaatctc aaaagcaaga ctcccaaaag 1380  
 gacgacaaca agcaattgcc atccgtcga aagaaaacg acgcgttcc tgaatccg 1440  
 aagggtgtt ctttggctac caagccaaact aagggtgaag ttgaatctt ctctactact 1500  
 ccaaccaagg ttgttccac tacccaaac gtcgctaagc caactaccgg ctcttccaag 1560  
 actaccaagg acgttgc aacttctgct gttcccttg aagctaagga ctctgctcca 1620  
 ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680  
 aacactcaag aaaacaaggc taagtcttaa 1710

<210> 42  
 <211> 481  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nI+

<400> 42  
 Met Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr  
 1 5 10 15  
 Glu Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr  
 20 25 30  
 Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala  
 35 40 45  
 Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala  
 50 55 60  
 Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn  
 65 70 75 80  
 Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro  
 85 90 95  
 Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp  
 100 105 110  
 Phe Glu Met Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala  
 115 120 125  
 Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu  
 130 135 140  
 Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val  
 145 150 155 160

Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr  
 165 170 175  
 Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys  
 180 185 190  
 Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys  
 195 200 205  
 Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala  
 210 215 220  
 Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala  
 225 230 235 240  
 Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn  
 245 250 255  
 Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys  
 260 265 270  
 Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala  
 275 280 285  
 Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp  
 290 295 300  
 Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu  
 305 310 315 320  
 Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu  
 325 330 335  
 Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp  
 340 345 350  
 Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp  
 355 360 365  
 Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys  
 370 375 380  
 Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr  
 385 390 395 400  
 Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys  
 405 410 415  
 Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala  
 420 425 430  
 Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro  
 435 440 445  
 Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys  
 450 455 460  
 Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly  
 465 470 475 480  
 Lys

<210> 43  
 <211> 1452  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Encodes SEQ ID NO: 42 and is codon optimized for  
 yeast expression

<400> 43  
 atggctgaag aaactggtgg taccAACACT gaagctcaac caaAGACCga agctgtcgct 60

tcccccaacca ctacctctga aaaggctcca gaaactaagc cagttctaa cgctgtctcc 120  
 gtttctaaca aggaagtctga agctccaacc tccgaaacta aggaagctaa ggaagtttaag 180  
 gaagtcaagg ctccaaagga aactaagaa gtcagccag ctgctaaggc taccaacaac 240  
 acttacccaa ttttgaacca agaattgaga gaagctatta agaaccgc tatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360  
 acccaacaat tctaccacta cgcgtccct gtcaagccag cttagttat tttcaccgac 420  
 tctaagccag aaatcgaatt gggtttgcac tccggtaat tctggagaaa gttcgaagtc 480  
 tacgaaggtg acaagaagtt gccaattaag ttgtttcct acgacaccgt caaggactac 540  
 gcttacatca gatttccgt ttctaacggc actaaggctg tcaagattgt ctcttccacc 600  
 cacttcaaca acaaggaaga aaagtacgac tacacttga tggattcgc tcaaccaatt 660  
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttgct 720  
 ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaaagacac caagaaggct 840  
 ttggacgaaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960  
 tccatgatgg acacccctcgtaa agcaccacca attaagactg gtatgttgcg cggtaagaag 1020  
 tacatggtca tggaaaccac taacgacgac tactggagg acttcatggc tgaaggtaaa 1080  
 agagtcagaa ccatctccaa ggacgctaa aacaacacta gaaccattat cttccatata 1140  
 gtgaaggta agactttgtc cgacgctatc gtcaagggttc acgtcaagac tattgactac 1200  
 gacggtaat accacgttag aattgttgcg aagaagctt tcaccaaggc taacaccgac 1260  
 aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320  
 ccatctaagc caaccccatc tccagttgaa aagaatctc aaaagcaaga ctcccaaaag 1380  
 gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440  
 aagtaaggat cc 1452

<210> 44  
 <211> 605  
 <212> PRT  
 <213> ORF0657nG

<400> 44

Met	Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr
1		5					10						15		
Glu	Ala	Val	Ala	Ser	Pro	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	
		20					25						30		
Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala
			35			40						45			
Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala
	50				55						60				
Pro	Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn
	65				70			75					80		
Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro
					85			90					95		
Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp
			100			105							110		
Phe	Glu	Met	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	
			115				120					125			
Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu
		130			135								140		
Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val
	145				150				155					160	
Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr
					165				170				175		
Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys
					180			185					190		

Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys  
 195 200 205  
 Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala  
 210 215 220  
 Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala  
 225 230 235 240  
 Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn  
 245 250 255  
 Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys  
 260 265 270  
 Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala  
 275 280 285  
 Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp  
 290 295 300  
 Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu  
 305 310 315 320  
 Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu  
 325 330 335  
 Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp  
 340 345 350  
 Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp  
 355 360 365  
 Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys  
 370 375 380  
 Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr  
 385 390 395 400  
 Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys  
 405 410 415  
 Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala  
 420 425 430  
 Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro  
 435 440 445  
 Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys  
 450 455 460  
 Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly  
 465 470 475 480  
 Lys Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser  
 485 490 495  
 Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala  
 500 505 510  
 Lys Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr  
 515 520 525  
 Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala  
 530 535 540  
 Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys  
 545 550 555 560  
 Asn Thr Gln Glu Asn Lys Ala Lys Ser Leu Pro Gln Thr Gly Glu Glu  
 565 570 575  
 Ser Asn Lys Asp Met Thr Leu Pro Leu Met Ala Leu Leu Ala Leu Ser  
 580 585 590  
 Ser Ile Val Ala Phe Val Leu Pro Arg Lys Arg Lys Asn  
 595 600 605

<211> 1818  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Encodes SEQ ID NO: 44 containing an amino terminus  
 methionine and is codon optimized for yeast  
 expression

<400> 45

```

atggctgaag aaactggtgg taccacact gaagctcaac caaagaccga agctgtcgt 60
tcccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccacaac 240
acttacccaa ttttgaacca agaattgaga gaagcttata agaaccacgc tatcaaggac 300
aaggaccact ccgcctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaaat tctaccacta cgcgtcctct gtcaagccag cttaggttat ttccaccgac 420
tctaagccag aaatcgaatt gggtttgc当地 tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaattaaat ttgtttcct acgcacccgt caaggactac 540
gcttacatca gatttccgt ttctaaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaaagacac caagaaggt 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgc当地 cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acacccctgt taagcacccca attaagactg gtatgttgc当地 cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggagg acttcatggt tgaaggtcaa 1080
agagtcaagaa cc当地tccaa ggacgctaa aacaacacta gaaccattat ctccc当地tac 1140
gttgaaggta agactttgtt cgc当地gtctac gtcaagggtt acgtcaagac tattgactac 1200
gacggtaat accacgttag aattgttgc当地 aaggaaagctt tcaccaaggc taacaccgac 1260
aagtccaaaca agaaggaaca acaagacaac tctgctaa a ggaagctac cccagctacc 1320
ccatctaaggc caaccccatc tccagttgaa aaggaaatctc aaaagcaaga ctcccaaag 1380
gacgacaaca agcaatttgc当地 atccgtc当地 aaggaaaacg acgc当地gtctt tgaatccgt 1440
aaggacaaga ctccagctac caagccaaact aagggttgc当地 ttgaatctt ctctactact 1500
ccaaaccagg ttgttccac tacccttccaa gtc当地gctaa cactaccgc ttcttccaa 1560
actaccaagg acgttgc当地 aacttctgt gttcctctg aagctaagga ctctgctcc 1620
ttgcaaaagg ctaacatcaa gaacaccaac gacggtc当地 cccaaatccc aaacaacaag 1680
aacactcaag aaaacaaggc taagtctttt ccacaaaccg gt当地agaatc caacaaggac 1740
atgaccttgc cattgatggc tttgttggc当地 ttgttccaa tcggttgc当地 cgttgc当地 1800
agaaagagaa agaactaa 1818
  
```

<210> 46  
 <211> 1710  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Encodes SEQ ID NO: 17 containing an amino terminus  
 methionine and is codon optimized for yeast  
 expression

<400> 46

```

atggctgaag aaactggtgg taccacact gaagctcaac caaagaccga agctttggc当地 60
tcccccaacca ctaccactga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
  
```

gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180  
 gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240  
 acttacccaa ttttgaacca agaattgaga gaagcttata agaaccgc tatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360  
 gaacaacaat tctaccacta cgcgtcctt gtcaagccag ctagagttat tttcaccgac 420  
 tctaagccag aaatcgaaatt gggtttgc当地 tccggtcaat tctggagaaa gttcgaagtc 480  
 tacgaagggt acaagaagtt gccaattaag ttggtttctt acgcacccgt caaggactac 540  
 gcttacatca gatttccgt ttcttaacggt actaaggctg tcaagattgt ctcttccacc 600  
 cacttcaaca acaagaaga aaagtacgac tacacttga tggaaattcgc tcaaccaatt 660  
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720  
 ccatacaaga aggctaaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaaagacac caagaaggct 840  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgc当地 cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960  
 tccatgatgg acacccctgt taagcacccaa attaagactg gtatgttgc当地 cggttaagaag 1020  
 tacatggtca tggaaaccac taacgacgac tactggagg acttcatgtt tgaaggtcaa 1080  
 agagtcagaa ccatctccaa ggacgctaa aacaacacta gaaccattat ctcccatac 1140  
 gttgaaggta agacttgc当地 cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200  
 gacggtaat accacgttag aattgttgc当地 aaggaaagctt tcaccaaggc taacaccgac 1260  
 aagtccaaaca agaagaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320  
 ccatctaagc caaccccatc tccagttgaa aagaatctc aaaagcaaga ctcccaaaag 1380  
 gacgacaaca agcaatttgc当地 atccgtc当地 aaggaaaacg acgcgtctt tgaatccggt 1440  
 aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatctt ctctactact 1500  
 ccaaccaagg ttgttccac tacccaaaac gtcgctaaagc caactaccgc ttcttccaaag 1560  
 actaccaagg acgttgc当地 aacttctgtt ggttccctg aagctaagga ctctgctcca 1620  
 ttgcaaaagg ctaacatcaa gaacaccaac gacggtc当地 cccaaatccca aaacaacaag 1680  
 aacactcaag aaaacaaggc taagtcttaa 1710

<210> 47  
 <211> 1446  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Encodes the SEQ ID NO: 17 I+ region, is codon optimized for yeast expression, and encodes a methionine initiation codon

<400> 47  
 atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttggct 60  
 tcccccaacca ctaccactga aaaggctcca gaaactaagc cagttctaa cgctgtctcc 120  
 gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180  
 gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240  
 acttacccaa ttttgaacca agaattgaga gaagcttata agaaccgc tatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360  
 gaacaacaat tctaccacta cgcgtcctt gtcaagccag ctagagttat tttcaccgac 420  
 tctaagccag aaatcgaaatt gggtttgc当地 tccggtcaat tctggagaaa gttcgaagtc 480  
 tacgaagggt acaagaagtt gccaattaag ttggtttctt acgcacccgt caaggactac 540  
 gcttacatca gatttccgt ttcttaacggt actaaggctg tcaagattgt ctcttccacc 600  
 cacttcaaca acaagaaga aaagtacgac tacacttga tggaaattcgc tcaaccaatt 660  
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720  
 ccatacaaga aggctaaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaaagacac caagaaggct 840  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgc当地 cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960

tccatgatgg acacccttcgt taagcaccca attaagactg gtatgttcaa cggttaagaag 1020  
 tacatggtca tggaaaccac taacgacgac tactggagg acttcatggt tgaaggtaa 1080  
 agagtcaaggaa ccatctccaa ggacgctaa aacaacacta gaaccattat cttccatac 1140  
 gttgaaggta agactttgtc cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200  
 gacggtcaat accacgttag aattgttgc aaggaagctt tcaccaaggc taacaccgac 1260  
 aagtccaaaca agaaggaaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320  
 ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380  
 gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtctc tgaatccgt 1440  
 aagtaa 1446

<210> 48  
 <211> 1341  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Encodes the SEQ ID NO: 17 I region, is codon optimized for yeast expression, and encodes a methionine initiation codon

<400> 48  
 atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttggct 60  
 tcccccaacca ctaccactga aaaggctcca gaaactaaggc cagttctaa cgctgtctcc 120  
 gtttctaaca aggaagtgcg agctccaacc tccgaaacta aggaagctaa ggaagttaa 180  
 gaagtcaagg ctccaaagga aactaaggct gtcaaggccag ctgctaaggc tgacaacaac 240  
 acttacccaa ttttgaacca agaattgaga gaagctatta agaaccaggc tatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aatgaagaa gaaaaacggt 360  
 gaacaacaat tctaccacta cgcgtccctc gtcaaggccag cttagattat tttcaccgac 420  
 tctaagccag aaatcgaatt gggtttgcaa tccggtaat tctggagaaa gttcgaagtc 480  
 tacgaagggtg acaagaagtt gccaattaaag ttggttcct acgacaccgt caaggactac 540  
 gcttacatca gattctccgt ttctaacgggt actaaggctg tcaagattgt ctcttccacc 600  
 cacttcaaca acaaggaaga aaagtacgac tacacttgc tggaaattcgc tcaaccaatt 660  
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720  
 ccatacaaga aggctaagac ttggaaaga caagtttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaaagacac caagaaggct 840  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgcaaga cactaagtac gtctgttacg aatccgtcga aaacaacgaa 960  
 tccatgatgg acacccttcgt taagcaccca attaagactg gtatgttcaa cggttaagaag 1020  
 tacatggtca tggaaaccac taacgacgac tactggagg acttcatggt tgaaggtaa 1080  
 agagtcaaggaa ccatctccaa ggacgctaa aacaacacta gaaccattat cttccatac 1140  
 gttgaaggta agactttgtc cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200  
 gacggtcaat accacgttag aattgttgc aaggaagctt tcaccaaggc taacaccgac 1260  
 aagtccaaaca agaaggaaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320  
 ccatctaagc caacccata a 1341

<210> 49  
 <211> 1938  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Encodes for full length ORF0657n containing SEQ ID NO: 17 modified to contain a glycine after the amino terminus methionine and is codon optimized for yeast expression

<400> 49

atgggttaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60  
 ggtgttgctt ctgtcgctat ctccacccctg ttgttgttga tgtctaaccg tgaagctcaa 120  
 gctgctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttggct 180  
 tcccccaacca ctaccactga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 240  
 gtttctaaca aggaagtcga agctccaacc tccgaaaacta aggaagctaa ggaagttaaag 300  
 gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 360  
 acttacccaa ttttgaacca agaattgaga gaagcttata agaaccaccg tatcaaggac 420  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaaaacggt 480  
 gaacaacaat tctaccacta cgcgtcctct gtcaagccag cttagagttat tttcaccgac 540  
 tctaagccag aaatcgaatt gggtttgc当地 tccggtaat tctggagaaa gttcgaagtc 600  
 tacgaaggtg acaagaagtt gccaatttaag ttgttccct acgacaccgt caaggactac 660  
 gcttacatca gattctccgt ttctaacggc actaaggctg tcaagattgt ctcttccacc 720  
 cacttcaaca acaaggaaga aaagtacgac tacacttga tggaaattcgc tcaaccaatt 780  
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 840  
 ccataacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 900  
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaaagacac caagaaggt 960  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 1020  
 aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 1080  
 tccatgatgg acacccctgt taagcacca attaagactg gtatgttgc当地 cggtaagaag 1140  
 tacatggtca tggaaaccac taacgacac tactggagg acttcatggt tgaaggtaa 1200  
 agagtcaagaa ccatctccaa ggacgctaaag aacaacacta gaaccattat cttccatata 1260  
 gttgaaggta agactttgtc cgacgctatc gtcaagggtt acgtcaagac tattgactac 1320  
 gacggtaat accacgttag aattgttgc当地 aaggaagctt tcaccaaggc taacaccgac 1380  
 aagtccaaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1440  
 ccatctaaggc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctccccaaaag 1500  
 gacgacaaca agcaattgcc atccgtc当地 aaggaaaacg acgcgtcttc tgaatccgg 1560  
 aaggacaaga ctccagctac caagccagct aagggttgc当地 ttgaatcttc ctctactact 1620  
 ccaaccaagg ttgtctccac tacccttccaaac gtcgctaaac caactaccgc ttcttccaa 1680  
 actaccaagg acgttgc当地 aacttctgtt ggttccctgt aagctaagga ctctgctcca 1740  
 ttgcaaaagg ctaacatcaa gaacaccaac gacggtc当地 cccaatcccc aaacaacaag 1800  
 aacactcaag aaaacaaggc taagtcttgc ccacaaaccg gtgaagaatc caacaaggac 1860  
 atgacccctgc cattgatggc tttgttggct ttgttccaa tcgttgc当地 cgttgc当地 1920  
 agaaagagaa agaactaa 1938

<210> 50

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 20, is codon optimized for yeast expression, and encodes a methionine initiation codon

<400> 50

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60  
 tcccccaacca ctacccctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120  
 gtttctaaca aggaagtcga agctccaacc tccgaaaacta aggaagctaa ggaagttaaag 180  
 gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240  
 acttacccaa ttttgaacca agaattgaga gaagcttata agaaccaccg tatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaaaacggt 360  
 gaacaacaat tctaccacta cgcgtcctct gtcaagccag cttagagttat tttcaccgac 420  
 tctaagccag aaatcgaatt gggtttgc当地 tccggtaat tctggagaaa gttcgaagtc 480

tacgaagggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540  
 gcttacatca gattctccgt ttctaacggg actaaggctg tcaagattgt ctcttccacc 600  
 cacttcaaca acaaggaaga aaagtacgac tacactttga tggattcgc tcaaccaatt 660  
 tacaactctg ctgacaagggtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720  
 ccataacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggagacac caagaaggct 840  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgcaga cactaagtac gtcgtctacg aatccgtcg aaacaacgaa 960  
 tccatgatgg acacccctcgtaa agtggaaaga caagtttacg aattgaacaa gatccaagac 1020  
 tacatggtca tggaaaccac taacgacac tactggagg acttcatgtt tgaaggtaaa 1080  
 agagtcaaggaa ccatctccaa ggacgcttaa aacaacacta gaaccattat ctcccatac 1140  
 gttgaaggta agactttgtc cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200  
 gacggtaat accacgttag aattgttgc aagaagctt tcaccaaggc taacaccgac 1260  
 aagtccaaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320  
 ccatctcaagc caaccccatc tccagttgaa aagaatctc aaaagcaaga ctcccaaaag 1380  
 gacgacaaca agcaattgcc atccgtcgaa aagaaaaacg acgcgtctc tgaatccgt 1440  
 aaggacaaga ctccagctac caagccagct aagggtgaaag ttgaatctc ctctactact 1500  
 ccaaccaagg ttgtctccac taccctaaac gtcgctaagc caactaccgc ttcttccaag 1560  
 actaccaagg acgttgc aacttctgtt ggtcctctg aagctaagga ctctgctcca 1620  
 ttgcaaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1680  
 aacactcaag aaaacaaggc taagtcttaa 1710

<210> 51  
 <211> 1446  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Encodes SEQ ID NO: 20 I+ region, is codon  
 optimized for yeast expression, and encodes a  
 methionine initiation codon

<400> 51  
 atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60  
 tcccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120  
 gtttctaaca aggaagtgcg agctccaacc tccgaaacta aggaagctaa ggaagttaa 180  
 gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240  
 acttacccaa ttttgaacca agaattgaga gaagctatta agaaccaccgac tatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaaaacggt 360  
 gaacaacaat tctaccacta cgcgtccctt gtcaagccag cttagagttat tttcaccgac 420  
 tctaagccag aaatcgaatt gggtttgc a tccggtaat tctggagaaa gttcgaagtc 480  
 tacgaagggtg acaagaagtt gccaattaag ttgtttcct acgacaccgt caaggactac 540  
 gcttacatca gattctccgt ttctaacggg actaaggctg tcaagattgt ctcttccacc 600  
 cacttcaaca acaaggaaga aaagtacgac tacactttga tggattcgc tcaaccaatt 660  
 tacaactctg ctgacaagggtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720  
 ccataacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggagacac caagaaggct 840  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgcaga cactaagtac gtcgtctacg aatccgtcg aaacaacgaa 960  
 tccatgatgg acacccctcgtaa agtggaaaga caagtttacg aattgaacaa gatccaagac 1020  
 tacatggtca tggaaaccac taacgacac tactggagg acttcatgtt tgaaggtaaa 1080  
 agagtcaaggaa ccatctccaa ggacgcttaa aacaacacta gaaccattat ctcccatac 1140  
 gttgaaggta agactttgtc cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200  
 gacggtaat accacgttag aattgttgc aagaagctt tcaccaaggc taacaccgac 1260  
 aagtccaaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320

ccatctaagg caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1380  
 gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccgg 1440  
 aagtaa 1446

<210> 52  
 <211> 1341  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Encodes the SEQ ID NO: 20 I region, is codon optimized for yeast expression, and encodes a methionine initiation codon

<400> 52  
 atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60  
 tcccccaacca ctacctctga aaaggctcca gaaactaaggc cagttgtctaa cgctgtctcc 120  
 gtttctaaca aggaagtgcg agctccaacc tccgaaacta aggaagctaa ggaagttaag 180  
 gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240  
 acttacccaa ttttgaacca agaattgaga gaagcttata agaaccacgc tatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaaaacgg 360  
 gaacaacaat tctaccacta cgcgtcctt gtcaagccag cttaggttat tttcaccgac 420  
 tctaagccag aaatcgaatt gggtttgc当地 tccggtaat tctggagaaa gttcgaagtc 480  
 tacgaagggtg acaagaagtt gccaattaag ttgtttctt acgacaccgt caaggactac 540  
 gtttacatca gatttccgt ttctaaacggt actaaggctg tcaagattgt ctcttccacc 600  
 cacttcaaca acaaggaaga aaagtacgac tacactttga tggaaattcgc tcaaccaatt 660  
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720  
 ccataacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaaagacac caagaaggct 840  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgc当地 cactaaggatc gtcgtctacg aatccgtcga aaacaacgaa 960  
 tccatgatgg acacccctgt taagcacca attaagactg gtatgttgc当地 cggtaagaag 1020  
 tacatggtca tggaaaccac taacgacgac tactggagg acttcatggt tgaaggtcaa 1080  
 agagtcagaa ccatctccaa ggacgctaa aacaacacta gaaccattat cttccatata 1140  
 gttgaaggta agactttgtt cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200  
 gacggtaat accacgttag aattgttgc当地 aaggaaagctt tcaccaaggc taacaccgac 1260  
 aagtccaaaca agaaggaaca acaagacaac tctgctaa aaggaaagctac cccagctacc 1320  
 ccatctaagg caaccccatc a 1341

<210> 53  
 <211> 1938  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Encodes for full length ORF0657n containing SEQ ID NO: 20 modified to contain a glycine after the amino terminus methionine and is codon optimized for yeast expression

<400> 53  
 atgggttaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60  
 ggtgttgc当地 ctgtcgctat ctccacctt当地 ttgttgc当地 tgc当地 taaacgg tgaagctcaa 120  
 gctgctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 180  
 tcccccaacca ctacctctga aaaggctcca gaaactaaggc cagttgtctaa cgctgtctcc 240

gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 300  
 gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 360  
 acttacccaa ttttgaacca agaattgaga gaagcttata agaaccacgc tatcaaggac 420  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 480  
 gaacaacaat tctaccacta cgcgtccctc gtcaagccag cttagagttat tttcaccgac 540  
 tctaagccag aaatcgatt gggtttgc当地 tccggtcaat tctggagaaa gttcgaagtc 600  
 tacgaaggtg acaagaagtt gccaattaag ttgtttccct acgacaccgt caaggactac 660  
 gcttacatca gatttccgt ttctaacggc actaaggctg tcaagattgt ctcttccacc 720  
 cacttcaaca acaaggaaga aaagtacgac tacacttga tggattcgc tcaaccaatt 780  
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttgct 840  
 ccatacaaga aggctaagac ttttggaaaga caagtttacg aattgaacaa gatccaagac 900  
 aagttgcccag aaaagttgaa ggctgaatac aagaagaagt tggaaagacac caagaaggct 960  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 1020  
 aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 1080  
 tccatgatgg acaccctcgtaa agcaccacca attaagactg gtatgttgcgtaagaag 1140  
 tacatggtca tggaaaccac taacgacac tactggagg acttcatgg tgaaggtcaa 1200  
 agagtcaagaa ccatctccaa ggacgctaaag aacaacacta gaaccattat cttccatata 1260  
 gttgaaggtt agactttgtt cgtacgttacgttcaagggtt acgtcaagac tattgactac 1320  
 gacggtaat accacgttag aatttgcgactt aagaagctt tcaccaaggc taacaccgac 1380  
 aagtccaaaca agaaggaaca acaagacaac tctgctaaag aagaagctac cccagctacc 1440  
 ccatctaagc caaccccatc tccagttgaa aagaatctc aaaagcaaga ctcccaaaag 1500  
 gacgacaaca agcaattgcc atccgtcgaa aagaaaacg acgcgtctc tgaatccgt 1560  
 aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1620  
 ccaaccaagg ttgtctccac taccctaaac gtcgctaaagc caactaccgc ttcttccaag 1680  
 actaccaagg acgttgc当地 aacttctgct ggttctctg aagctaagga ctctgctcca 1740  
 ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccatccaa aaacaacaag 1800  
 aacactcaag aaaacaaggc taagtcttg ccacaaaccg gtgaagaatc caacaaggac 1860  
 atgaccttgc cattgatggc tttgttgct ttgtcttcca tcgttgcttt cgtcttgcca 1920  
 agaaaagagaaa agaactaa 1938

&lt;210&gt; 54

&lt;211&gt; 565

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 54

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1															
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys
	20														
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
	35														
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr
	50														
Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile
	65														
Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp
	85														
Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys
	100														
Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys
	115														

Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly  
 130 135 140  
 Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp  
 145 150 155 160  
 Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr  
 165 170 175  
 Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile  
 180 185 190  
 Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr  
 195 200 205  
 Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys  
 210 215 220  
 Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys  
 225 230 235 240  
 Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp  
 245 250 255  
 Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Leu Glu Asp  
 260 265 270  
 Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe  
 275 280 285  
 Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr  
 290 295 300  
 Lys Tyr Ala Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp  
 305 310 315 320  
 Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys  
 325 330 335  
 Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met  
 340 345 350  
 Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn  
 355 360 365  
 Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp  
 370 375 380  
 Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr  
 385 390 395 400  
 His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp  
 405 410 415  
 Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala  
 420 425 430  
 Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu  
 435 440 445  
 Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser  
 450 455 460  
 Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr  
 465 470 475 480  
 Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr  
 485 490 495  
 Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr  
 500 505 510  
 Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser  
 515 520 525  
 Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn  
 530 535 540  
 Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu  
 545 550 555 560

Asn Lys Ala Lys Ser  
565

<210> 55  
<211> 568  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> ORF0657nH

<400> 55  
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
1 5 10 15  
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
20 25 30  
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
35 40 45  
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
50 55 60  
Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
65 70 75 80  
Tyr Pro Ile Leu Asn Gln Gly Leu Arg Glu Ala Ile Lys Asn Pro Ala  
85 90 95  
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
100 105 110  
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser  
115 120 125  
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
130 135 140  
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
145 150 155 160  
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
165 170 175  
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
180 185 190  
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
195 200 205  
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
210 215 220  
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
225 230 235 240  
Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
245 250 255  
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
260 265 270  
Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Pro Ala Ile  
275 280 285  
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
290 295 300  
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
305 310 315 320  
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
325 330 335

<210> 56  
<211> 568  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> ORF0657nH

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<400> 56
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
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Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
  20          25          30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
  35          40          45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
  50          55          60
Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
  65          70          75          80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Glu
  85          90          95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
 100         105         110

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Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160  
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Ile Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Val Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540

Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

<210> 57  
 <211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<220>  
 <221> SITE  
 <222> 247  
 <223> Unknown

<400> 57  
 Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Pro Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Thr Lys Asn Pro Glu  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Thr Asp Phe  
 100 105 110  
 Glu Met Lys Lys Asn Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160  
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Ile Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Xaa Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270

Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Leu Leu Lys Thr His Asp Gly His Thr Gln Ser Gln Asn Ile Lys Asn  
 545 550 555 560  
 Thr Lys Lys Asp Lys Ala Lys Ser  
 565

<210> 58  
 <211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 58  
 Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45

Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Glu Asn Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160  
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480

Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	Ser
485									490					495	
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys
500									505					510	
Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser
515									520					525	
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn
530									535					540	
Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn
545									550					560	
Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser								
					565										

<210> 59  
<211> 567  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> ORF0657nH

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys
									25					30	
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
									40					45	
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
									55					60	
Lys	Glu	Thr	Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr
									70					80	
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
									85					95	
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
									100					110	
Glu	Met	Asn	Lys	Lys	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
									115					125	
Ser	Ala	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
									130					140	
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
									145					160	
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
									165					175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
									180					190	
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Asp
									195					205	
Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys
									210					220	
Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr
									225					240	
Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile
									245					255	

Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu  
 260 265 270  
 Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr  
 275 280 285  
 Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln  
 290 295 300  
 Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met  
 305 310 315 320  
 Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly  
 325 330 335  
 Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp  
 340 345 350  
 Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys  
 355 360 365  
 Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu  
 370 375 380  
 Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly  
 385 390 395 400  
 Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn  
 405 410 415  
 Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys  
 420 425 430  
 Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu  
 435 440 445  
 Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu  
 450 455 460  
 Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp  
 465 470 475 480  
 Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser Ser  
 485 490 495  
 Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro  
 500 505 510  
 Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala  
 515 520 525  
 Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile  
 530 535 540  
 Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr  
 545 550 555 560  
 Gln Glu Asn Lys Ala Lys Ser  
 565

<210> 60  
 <211> 576  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 60  
 Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala  
 20 25 30

Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys  
 35 40 45  
 Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys  
 50 55 60  
 Ala Val Lys Glu Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro  
 65 70 75 80  
 Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu  
 85 90 95  
 Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala  
 100 105 110  
 Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr  
 115 120 125  
 Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile  
 130 135 140  
 Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln  
 145 150 155 160  
 Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile  
 165 170 175  
 Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe  
 180 185 190  
 Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His  
 195 200 205  
 Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala  
 210 215 220  
 Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr  
 225 230 235 240  
 Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu  
 245 250 255  
 Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys  
 260 265 270  
 Leu Lys Ala Glu Tyr Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu  
 275 280 285  
 Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro  
 290 295 300  
 Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Ala Tyr  
 305 310 315 320  
 Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His  
 325 330 335  
 Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu  
 340 345 350  
 Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg  
 355 360 365  
 Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile  
 370 375 380  
 Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val  
 385 390 395 400  
 His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val  
 405 410 415  
 Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys  
 420 425 430  
 Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro  
 435 440 445  
 Ser Lys Pro Thr Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp  
 450 455 460

Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Ser	Pro	Ser	Val	Glu	Lys	Glu	Asn
465															480
Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Met	Pro	Val	Thr	Lys	Pro
															495
Ala	Lys	Ala	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val
															510
Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Glu	Thr
															525
Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp
															540
Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His
545															560
Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser
															575

<210> 61  
 <211> 572  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Ser	Pro	Ser	Val	Glu	Lys	Glu	Asn
1															15
Ala	Glu	Glu	Thr	Gly	Val	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	
															30
Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Val	Ala
															45
Pro	Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Val	Lys	Glu
Val	Lys	Ala	Pro	Lys	Glu	Ala	Lys	Glu	Glu	Lys	Pro	Ala	Ala	Lys	Ala
65															80
Asp	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile
															95
Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg
															110
Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	
															125
His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser
															140
Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys
145															160
Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser
															175
Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn
															190
Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys
															205
Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr
210															220
Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys
225															240

Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr  
 245 250 255  
 Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu  
 260 265 270  
 Tyr Lys Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val  
 275 280 285  
 Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys  
 290 295 300  
 Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu  
 305 310 315 320  
 Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr  
 325 330 335  
 Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp  
 340 345 350  
 Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile  
 355 360 365  
 Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Cys Val  
 370 375 380  
 Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr  
 385 390 395 400  
 Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala  
 405 410 415  
 Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys Glu Gln Gln Asp  
 420 425 430  
 Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro Ser Lys Pro Thr  
 435 440 445  
 Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp  
 450 455 460  
 Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser  
 465 470 475 480  
 Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro Ala Lys Ala Glu  
 485 490 495  
 Val Glu Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln  
 500 505 510  
 Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr Thr Lys Asp Val  
 515 520 525  
 Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu  
 530 535 540  
 Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln  
 545 550 555 560  
 Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 565 570

<210> 62  
 <211> 572  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 62  
 Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15

Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala  
 20 25 30  
 Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Val Ala  
 35 40 45  
 Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Val Lys Glu  
 50 55 60  
 Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro Ala Ala Lys Ala  
 65 70 75 80  
 Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile  
 85 90 95  
 Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg  
 100 105 110  
 Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr  
 115 120 125  
 His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser  
 130 135 140  
 Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys  
 145 150 155 160  
 Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser  
 165 170 175  
 Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn  
 180 185 190  
 Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys  
 195 200 205  
 Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr  
 210 215 220  
 Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys  
 225 230 235 240  
 Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr  
 245 250 255  
 Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu  
 260 265 270  
 Tyr Lys Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val  
 275 280 285  
 Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys  
 290 295 300  
 Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu  
 305 310 315 320  
 Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr  
 325 330 335  
 Gly Met Leu Asn Gly Lys Tyr Met Val Met Glu Thr Thr Asn Asp  
 340 345 350  
 Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile  
 355 360 365  
 Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val  
 370 375 380  
 Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr  
 385 390 395 400  
 Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala  
 405 410 415  
 Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys Glu Gln Gln Asp  
 420 425 430  
 Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro Ser Lys Pro Thr  
 435 440 445

Thr	Pro	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp
450				455					460						
Asp	Asn	Lys	Gln	Ser	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser
465				470				475							480
Glu	Ser	Gly	Lys	Asp	Lys	Met	Pro	Val	Thr	Lys	Pro	Ala	Lys	Ala	Glu
				485				490							495
Val	Glu	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	
				500			505				510				
Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Glu	Thr	Thr	Lys	Asp	Val
				515			520				525				
Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu
				530			535				540				
Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln
				545			550				555				560
Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser				
				565				570							

&lt;210&gt; 63

&lt;211&gt; 566

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 63

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5				10						15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	
				20			25							30	
Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Val	Ala
				35			40							45	
Pro	Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu
				50			55							60	
Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro
				65			70				75				80
Ile	Leu	Asn	Lys	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys
				85			90							95	
Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met
				100			105							110	
Lys	Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val
				115			120							125	
Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu
				130			135							140	
Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly
				145			150				155				160
Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp
				165			170							175	
Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys
				180			185							190	
Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr
				195			200							205	
Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe
				210			215							220	

Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys  
 225 230 235 240  
 Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln  
 245 250 255  
 Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu  
 260 265 270  
 Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu  
 275 280 285  
 Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp  
 290 295 300  
 Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met  
 305 310 315 320  
 Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys  
 325 330 335  
 Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe  
 340 345 350  
 Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn  
 355 360 365  
 Asn Thr Arg Thr Ile Ile Phe Pro Tyr Ile Glu Gly Lys Thr Leu Tyr  
 370 375 380  
 Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln  
 385 390 395 400  
 Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala  
 405 410 415  
 Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu  
 420 425 430  
 Thr Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Pro Pro Val Glu Lys  
 435 440 445  
 Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Thr Gln Ser Pro  
 450 455 460  
 Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys  
 465 470 475 480  
 Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Thr  
 485 490 495  
 Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr  
 500 505 510  
 Thr Ala Ser Ser Glu Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly  
 515 520 525  
 Pro Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys  
 530 535 540  
 Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln  
 545 550 555 560  
 Glu Asp Lys Ala Lys Ser  
 565

<210> 64  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> His-Tag

<400> 64

Leu Glu His His His His His His  
 1 5

<210> 65  
 <211> 16  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 65  
 ctggccgtcg ttttac

16

<210> 66  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 66  
 caggaaacag ctagac

17

<210> 67  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 67  
 aaccggtttt ccatggggaa caaacagcaa aaagaattt

39

<210> 68  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 68  
 acccggttct cgagggtttt acgtttctta ggtaatac

38

<210> 69  
 <211> 109  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> ORF0657n oligomer

<400> 69  
atgggtaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60  
ggtgttgctt ctgtcgctat ctccaccttg ttgttgttga tgtctaacg 109

<210> 70  
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<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 70  
gttgggaag cgacagcttc ggtctttggc tgagcttcag tgggttacc accagttct 60  
tcagcagcag cttgagcttc accgttagac atcaacaaca acaagggtgga 110

<210> 71  
<211> 110  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 71  
agaccgaagc tgcgtttcc ccaaccacta cctctgaaaa ggctccagaa actaagccag 60  
ttgcttaacgc tgcgtccgtt tctaacaagg aagtcgaagc tccaaacctcc 110

<210> 72  
<211> 109  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 72  
tggtaggcctt agcagctggc ttgacttcct tagttcctt tggagccttg acttccttaa 60  
cttccttagc ttcccttagtt tcggaggttg gagcttcgac ttcccttggtt 109

<210> 73  
<211> 108  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> ORF0657n oligomer

<400> 73  
aagtcaagcc agctgctaag gctaccaaca acacttaccc aattttgaac caagaattga 60  
gagaagctat taagaaccca gctatcaagg acaaggacca ctcccgctc 108

<210> 74  
<211> 109

<212> DNA  
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<220>  
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<400> 74  
tggcttgaca gaggacgcgt agtggtagaa ttgttggta ccgtccttct tcttcatttc 60  
gaagtgcatt ggtctagagt ttggagcgg a gtggcccttg tccttgata 109

<210> 75  
<211> 102  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> ORF0657n oligomer

<400> 75  
accactacgc gtcctctgtc aagccagcta gagttatttt caccgactct aagccagaaa 60  
tcgaattggg tttgcaatcc ggtcaattct ggagaaaagtt cg 102

<210> 76  
<211> 104  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> ORF0657n oligomer

<400> 76  
ctgatgttaag cgtagtcctt gacgggtgtcg taggaaacca acttaattgg caacttcttg 60  
tcacccctcgat agacttcgaa ctttctccag aattgaccgg attg 104

<210> 77  
<211> 109  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> ORF0657n oligomer

<400> 77  
caccgtcaag gactacgctt acatcagatt ctccgtttct aacggtaacta aggctgtcaa 60  
gattgtctct tccacccact tcaacaacaa ggaagaaaag tacgactac 109

<210> 78  
<211> 109  
<212> DNA  
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<220>  
<223> ORF0657n oligomer

<400> 78

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aactttcag cctttagtc ttcttcggc ttgaacttgt cagcagagtt gtaaattgg 60
tgagcgaatt ccatcaaagt gtagtcgtac tttcttcct tgggttga 109

<210> 79
<211> 106
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF0657n oligomer

<400> 79
ccgaagaaga ctacaaggct gaaaagggtt tggctccata caagaaggct aagactttgg 60
aaagacaagt ttacgaattt aacaagatcc aagacaagtt gccaga 106

<210> 80
<211> 109
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF0657n oligomer

<400> 80
tcggtgatacg cggacttgac ttgttcgtcc aaagccttct tgggtgtcttc caacttcttc 60
ttgtattcag cttcaactt ttctggcaac ttgtcttggaa tcttggta 109

<210> 81
<211> 109
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF0657n oligomer

<400> 81
cgaacaaggctc aagtccgcta tcaccgaatt ccaaaacgtt caaccaacta acgaaaagat 60
gactgacttg caagacacta agtacgtcgt ctacgaatcc gtcgaaaac 109

<210> 82
<211> 109
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF0657n oligomer

<400> 82
tttccatgac catgtacttc ttaccgttca acataccagt cttaattggg tgcttaacga 60
aggtgtccat catggattcg ttgtttcga cggattcgtt gacgacgtt 109

<210> 83
<211> 109
<212> DNA
<213> Artificial Sequence

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<220>
<223> ORF0657n oligomer

<400> 83
gaacggtaag aagtacatgg tcatggaaac cactaacgac gactactgga aggacttcat 60
gttgaaggt caaagagtca gaaccatctc caaggacgct aagaacaac 109

<210> 84
<211> 101
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF0657n oligomer

<400> 84
gtttgacgt gaaccttgac gatagcgtcg tacaaggatct taccttcaac gtatggaaag 60
ataatggttc tagtgttctt ctagcgtcc ttggagatgg t 101

<210> 85
<211> 106
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF0657n oligomer

<400> 85
cgctatcgtc aaggttcacg tcaagactat tgactacgac ggtcaataacc acgttagaat 60
tggacaag gaagcttca ccaaggctaa caccgacaag tccaac 106

<210> 86
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF0657n oligomer

<400> 86
tgggttggc ttagatgggg tagctgggtt agcttccttc ttagcagagt tgcgttgg 60
ttcccttcttg ttggacttgtt cgggttagc cttgg 96

<210> 87
<211> 85
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF0657n oligomer

<400> 87
cagctacccc atctaagcca accccatctc cagttgaaaa ggaatctcaa aagcaagact 60
cccaaaagga cgacaacaag caatt 85

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<210> 88  
<211> 100  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> ORF0657n oligomer

<400> 88  
gttggcttgg tagctggagt cttgtcctta ccggattcag aagacgcgtc gttttccttt 60  
tcgacggatg gcaattgctt gttgtcgcc ttttgggagt 100

<210> 89  
<211> 101  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> ORF0657n oligomer

<400> 89  
ggacaagact ccagctacca agccaactaa gggtaagtt gaatcttcct ctactactcc 60  
aaccaagggtt gtctccacta cccaaaacgt cgctaagcca a 101

<210> 90  
<211> 101  
<212> DNA  
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<220>  
<223> ORF0657n oligomer

<400> 90  
acgagagtcc ttagcttcag aggaaccagc agaagttgg acaacgtcct tggtagtctt 60  
ggaagaagcg gtagttggct tagcgacgtt ttggtagtg g 101

<210> 91  
<211> 91  
<212> DNA  
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<220>  
<223> ORF0657n oligomer

<400> 91  
ggttcctctg aagctaagga ctctgctcca ttgcaaaagg ctaacatcaa gaacaccaac 60  
gacggtcaca cccaatccca aaacaacaag a 91

<210> 92  
<211> 98  
<212> DNA  
<213> Artificial Sequence

<220>

<223> ORF0657n oligomer  
 <400> 92  
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 tcgttgcttt cgtcttgcca agaaagagaa agaactaa 98  
 <210> 93  
 <211> 98  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
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 tcgttgcttt cgtcttgcca agaaagagaa agaactaa 98  
  
 <210> 94  
 <211> 31  
 <212> DNA  
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 <220>  
 <223> Primer  
  
 <400> 94  
 cttaaagctt atgtcaacttt ctcttgatc g 31  
  
 <210> 95  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primer  
  
 <400> 95  
 tgataagctt gctcaatggc tctcttcctc 30  
  
 <210> 96  
 <211> 53  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primer  
  
 <400> 96  
 aaccggtttg gatcccacaa aacaaaatgg gtaacaagca aacaaaaggaa ttc 53  
  
 <210> 97  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>		
<223> Primer		
<400> 97		42
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<210> 98		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
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<223> Primer		
<400> 98		24
gctgaagaaa ctgggtggac caac		
<210> 99		
<211> 42		
<212> DNA		
<213> Artificial Sequence		
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gtcacggatc cttaagactt agccttgttt tcttgagtgt tc		
<210> 100		
<211> 41		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Primer		
<400> 100		41
ggggggatcc cacaaaacaa aatggctgaa gaaactggtg g		
<210> 101		
<211> 39		
<212> DNA		
<213> Artificial Sequence		
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<223> Primer		
<400> 101		39
ggggggggat ccttaagact tagccttggtt ttcttgagt		
<210> 102		
<211> 41		
<212> DNA		
<213> Artificial Sequence		

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<220>
<223> Primer

<400> 102
ggggggatcc cacaaaacaa aatggctgaa gaaactggtg g 41

<210> 103
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 103
gggggggatc ctttagttctt tctctttctt gg 32

<210> 104
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 104
ctccggatcc cacaaaacaa aatggctgaa gaaactgg 39

<210> 105
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 105
gctgccggga tccttatggg gttggcttag atggggta 38

<210> 106
<211> 644
<212> PRT
<213> S. aureus

<400> 106
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
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Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu
 20          25          30
Met Ser Asn Gly Glu Ala Gln Ala Ala Glu Glu Thr Gly Gly Thr Asn
 35          40          45
Thr Glu Ala Gln Pro Lys Thr Glu Ala Leu Ala Ser Pro Thr Thr Thr
 50          55          60

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Thr Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser Val  
 65 70 75 80  
 Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys  
 85 90 95  
 Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Ala Val Lys Pro  
 100 105 110  
 Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu  
 115 120 125  
 Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala  
 130 135 140  
 Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Glu Asn Gly Glu  
 145 150 155 160  
 Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile  
 165 170 175  
 Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln  
 180 185 190  
 Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile  
 195 200 205  
 Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe  
 210 215 220  
 Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His  
 225 230 235 240  
 Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala  
 245 250 255  
 Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr  
 260 265 270  
 Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu  
 275 280 285  
 Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys  
 290 295 300  
 Leu Lys Ala Glu Tyr Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu  
 305 310 315 320  
 Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro  
 325 330 335  
 Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr  
 340 345 350  
 Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His  
 355 360 365  
 Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu  
 370 375 380  
 Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg  
 385 390 395 400  
 Val Arg Thr Ile Ser Lys Asp Ala Ile Asn Asn Thr Arg Thr Ile Ile  
 405 410 415  
 Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val  
 420 425 430  
 His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val  
 435 440 445  
 Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys  
 450 455 460  
 Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro  
 465 470 475 480  
 Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln Asp  
 485 490 495

Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu Asn  
 500 505 510  
 Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys Pro  
 515 520 525  
 Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val  
 530 535 540  
 Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys Thr  
 545 550 555 560  
 Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp  
 565 570 575  
 Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His  
 580 585 590  
 Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 595 600 605  
 Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro Leu  
 610 615 620  
 Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro Arg  
 625 630 635 640  
 Lys Arg Lys Asn

<210> 107  
 <211> 644  
 <212> PRT  
 <213> S. aureus

<400> 107  
 Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys  
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 Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu  
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 Met Ser Asn Gly Glu Ala Gln Ala Ala Glu Glu Thr Gly Gly Thr Asn  
 35 40 45  
 Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr Thr  
 50 55 60  
 Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser Val  
 65 70 75 80  
 Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys  
 85 90 95  
 Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Ala Val Lys Pro  
 100 105 110  
 Ala Thr Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu  
 115 120 125  
 Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala  
 130 135 140  
 Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Glu Asn Gly Glu  
 145 150 155 160  
 Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile  
 165 170 175  
 Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln  
 180 185 190  
 Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile  
 195 200 205

Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe  
 210 215 220  
 Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His  
 225 230 235 240  
 Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala  
 245 250 255  
 Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr  
 260 265 270  
 Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu  
 275 280 285  
 Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys  
 290 295 300  
 Leu Lys Ala Glu Tyr Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu  
 305 310 315 320  
 Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro  
 325 330 335  
 Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr  
 340 345 350  
 Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His  
 355 360 365  
 Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu  
 370 375 380  
 Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg  
 385 390 395 400  
 Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile  
 405 410 415  
 Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val  
 420 425 430  
 His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val  
 435 440 445  
 Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys  
 450 455 460  
 Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro  
 465 470 475 480  
 Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln Asp  
 485 490 495  
 Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu Asn  
 500 505 510  
 Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys Pro  
 515 520 525  
 Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val  
 530 535 540  
 Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys Thr  
 545 550 555 560  
 Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp  
 565 570 575  
 Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His  
 580 585 590  
 Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 595 600 605  
 Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro Leu  
 610 615 620  
 Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro Arg  
 625 630 635 640  
 Lys Arg Lys Asn

<210> 108  
<211> 5  
<212> PRT  
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<220>  
<223> cell wall sorting signal

<220>  
<221> SITE  
<222> 3  
<223> Xaa = any amino acid

<400> 108  
Leu Pro Xaa Thr Gly  
1 5

<210> 109  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> cell wall sorting signal

<220>  
<221> SITE  
<222> 3  
<223> Xaa = any amino acid

<400> 109  
Leu Pro Xaa Thr Gly Val Ile  
1 5